

## Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension **.rup**) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

**When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.**

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GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: February 27, 2006, 17:31:21 ; Search time 188 Seconds  
(without alignments)  
1269.057 Million cell updates/sec

Title: US-10-676-079-2

Perfect score: 2842

Sequence: 1 MLRSKPALPPMLLLLP.....LPAFSYFFVIRNAKVAACI 543

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A\_Geneseq\_21:\*

- 1: Geneseq1980s:\*
- 2: Geneseq1990s:\*
- 3: Geneseq2000s:\*
- 4: Geneseq2001s:\*
- 5: Geneseq2002s:\*
- 6: Geneseq2003as:\*
- 7: Geneseq2003bs:\*
- 8: Geneseq2004s:\*
- 9: Geneseq2005s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	2842	100.0	543	2 AAY02345	Aay02345 A human h
2	2842	100.0	543	3 AAY57590	Aay57590 Human hep
3	2842	100.0	543	3 AAB08849	Aab08849 Amino aci
4	2842	100.0	543	3 AAY52990	Aay52990 Human hep
5	2842	100.0	543	4 AAY97635	Aay97635 Human hep
6	2842	100.0	543	5 ABB07813	Abb07813 Human hep
7	2842	100.0	543	7 ADG88800	Adg88800 Human hpa
8	2842	100.0	543	8 ADL16379	Adl16379 Human hep
9	2842	100.0	543	8 ADM48716	Adm48716 Human hpa
10	2842	100.0	543	9 AEA42466	Aea42466 Human hep
11	2842	100.0	592	2 AAY02346	Aay02346 A human h
12	2842	100.0	592	3 AAB08850	Aab08850 Amino aci
13	2842	100.0	592	7 ADG88804	Adg88804 Human SK-
14	2842	100.0	592	8 ADL16383	Adl16383 Human hep
15	2842	100.0	592	8 ADM48720	Adm48720 Human SK-
16	2842	100.0	592	9 AEA42461	Aea42461 Human hep
17	2838	99.9	543	2 AAY17082	Aay17082 Human hep
18	2838	99.9	543	4 AAB86206	Aab86206 Human hep
19	2838	99.9	543	7 ADD18950	Add18950 Human dis
20	2838	99.9	543	8 ADK52086	Adk52086 Human ato
21	2838	99.9	543	8 ADM48759	Adm48759 Human hpa
22	2838	99.9	543	8 ADN05074	Adn05074 Antipsori
23	2838	99.9	543	8 ADN04902	Adn04902 Antipsori
24	2838	99.9	543	8 ADQ80372	Adq80372 Heparanas

#### ALIGNMENTS

RESULT 1

AAY02345

ID AAY02345 standard; protein; 543 AA.

XX AC AAY02345;

DT 09-JUL-1999 (first entry)

DE A human heparanase protein.

XX

Heparanase; hp; modulator; heparin-binding growth factor;  
cellular response; cytokine; cell interaction; plasma lipoprotein;  
cellular susceptibility; infection; disintegration;  
neurodegenerative plaque; wound healing; angiogenesis; restenosis;  
atherosclerosis; inflammation; neurodegenerative disease; neutralise;  
plasma heparin; micrometastasis; autoimmune lesion; renal failure.

XX Homo sapiens.

XX

PN WO9911798-A3-

XX 11-MAR-1999.

PD

XX 31-AUG-1998; 98WO-US017954.

XX

PR 02-SEP-1997; 97US-00922170.

PR 02-JUL-1998; 98US-00109386.

XX (INSI-) INSIGHT STRATEGY & MARKETING LTD.

PA (HADA-) HADASIT MEDICAL RES SERVICES & DEV.

PA (FRIE/) FRIEDMAN M.M.

XX Pecker I, Vlodavsky I, Feinstein E;

PI

XX WPI; 1999-302255/25.

DR N-PSDB; AAX35648.

XX

PT New human polynucleotide useful for treating angiogenesis, restenosis,  
PT and inflammation.

XX Claim 6; Fig 1; 63pp; English.

XX

CC The specification describes a polypeptide having heparanase (hp)  
CC activity. The recombinant protein is used as a modulator of heparin-  
CC binding growth factors, cellular responses to heparin-binding growth  
CC factors and cytokines, cell interaction with plasma lipoproteins,  
CC cellular susceptibility to viral, protozoal and bacterial infections or

Adr88210 Human pre  
Adp25079 PRO poly  
Adt78177 Human hep  
Aby27036 Human hep  
Aea42426 Human hep  
Aay30124 A human p  
Ado63831 Human hep  
Ado63823 Human hep  
Ado63832 Human hep  
Ado63822 Human hep  
Aab88361 Human mem  
Ado63824 Human hep  
Ady63087 Human clo  
Adz19010 Heparanas  
Adb56822 Human hep  
Ade16012 G-coupled  
Adl93951 Human G-c  
Adz19008 Heparanas  
Aay34173 Human pre  
Aay17083 Seq ID No  
Adz19004 HepGS4 Co

CC disintegration of neurodegenerative plaques. Heparanase may be useful for  
CC conditions such as wound healing, angiogenesis, restenosis,  
CC atherosclerosis, inflammation, neurodegenerative diseases, and viral  
CC infections. Mammalian heparanase can be used to neutralize plasma  
CC heparin, and anti-heparanase antibodies may be applied for  
CC immunodetection and diagnosis of micrometastases, autoimmune lesions, and  
CC renal failure in biopsy specimens, plasma samples, and body fluids. The  
CC present sequence represents human heparanase  
XX  
SQ Sequence 543 AA;

Query Match 100.0%; Score 2842; DB 2; Length 543;  
Best Local Similarity 100.0%; Pred. No. 2.9e-273;  
Matches 543; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLLRSKPALPPPLMLLLGPGPLSPGALPPAQADVVLDFFTOEPLHLVSPSFLSVT 60  
Db 1 MLLRSKPALPPPLMLLLGPGPLSPGALPPAQADVVLDFFTOEPLHLVSPSFLSVT 60  
Qy 61 IDANLATDPRFLILLGSPKLTARGLSPAYLRFGGKTDFLIIDPKKESFEERSYQWS 120  
Db 61 IDANLATDPRFLILLGSPKLTARGLSPAYLRFGGKTDFLIIDPKKESFEERSYQWS 120  
Qy 121 QVNQDICKYGIIPPDVEEKLREWPYQQLLREHYQKKFNSTYSRSSVDVLYTFANC 180  
Db 121 QVNQDICKYGIIPPDVEEKLREWPYQQLLREHYQKKFNSTYSRSSVDVLYTFANC 180  
Qy 181 GLDLIFGLNALLRTADLOWNSSNAQLLLDYCSSKGYNISWELGNEPNSFLKADIFINGS 240  
Db 181 GLDLIFGLNALLRTADLOWNSSNAQLLLDYCSSKGYNISWELGNEPNSFLKADIFINGS 240  
Qy 241 QLGEDYIQLHKLKRSKTFKNAKLYGPDVGQPRRTAKMLKSLKAGGVIDSVTWHYYL 300  
Db 241 QLGEDYIQLHKLKRSKTFKNAKLYGPDVGQPRRTAKMLKSLKAGGVIDSVTWHYYL 300  
Qy 301 NGRTATREDFLNPVDLDFISSVQKVFQVVESTRPGKKVWLGETSSAYGGGAPLLSDTFA 360  
Db 301 NGRTATREDFLNPVDLDFISSVQKVFQVVESTRPGKKVWLGETSSAYGGGAPLLSDTFA 360  
Qy 361 AGFWMLDKLGLSARMGIEVVMRQVFPFGAGNHLVDENFDPLPDYWLKLLFKLVGTVKVL 420  
Db 361 AGFWMLDKLGLSARMGIEVVMRQVFPFGAGNHLVDENFDPLPDYWLKLLFKLVGTVKVL 420  
Qy 421 ASVGSKRKLRLVYLHCTNTDNPRYKEGDLTIYALNLHNVTKYLRLPYPSNKQVDKYL 480  
Db 421 ASVGSKRKLRLVYLHCTNTDNPRYKEGDLTIYALNLHNVTKYLRLPYPSNKQVDKYL 480  
Qy 481 RPLGPHGLLSKSVQLNGLTLKXVDDQTLPLMEKPLRPGSSILGUPAFYSFFVIRNAKVA 540  
Db 481 RPLGPHGLLSKSVQLNGLTLKXVDDQTLPLMEKPLRPGSSILGUPAFYSFFVIRNAKVA 540  
Qy 541 ACI 543  
Db 541 ACI 543

RESULT 2  
AAV57590

ID AAV57590 standard; protein; 543 AA.

XX

AC AAV57590;

XX

DT 02-MAR-2000 (first entry)

XX

DE Human heparanase.

XX

KW Human; heparanase; hpa; genetic modification; expression; anticancer;  
KW angiogenesis; anti-angiogenic; antiproliferative; antiviral; antitumour;  
KW anti-atherosclerotic; anti-inflammatory; antineurodegeneration;  
KW heparan sulphate; heparin-binding growth factor; tumour angiogenesis;  
KW metastasis; wound healing; restenosis; atherosclerosis; inflammation;  
KW neurodegeneration; viral infection; cystic fibrosis; cancer; diagnosis;  
KW micrometastasis; autoimmune lesion; kidney failure.

XX Homo sapiens.  
OS  
XX  
PN WO9957244-A1.  
XX  
PD 11-NOV-1999.  
XX  
XX 29-APR-1999; 99WO-US009256.  
PR  
XX 01-MAY-1998; 98US-00071618.  
PR 02-MAR-1999; 99US-00260038.  
XX  
PA (INSI-) INSIGHT STRATEGY & MARKETING LTD.  
PA (FRIE/) FRIEDMAN M M.  
XX  
PI Ben-Artzi H, Ayal-Hershkovitz M, Yacoby-Zeevi O, Pecker I;  
PI Peleg Y, Shlomi Y;  
XX  
DR WPI; 2000-062144/05.  
DR N-PSDB; AAZ39195.  
XX  
XX Engineered cells that express recombinant heparanase, useful  
PT therapeutically, e.g. for treating angiogenesis and to screen for  
PT specific inhibitors, potential anticancer agents.  
XX  
PS Claim 3; Page 107-109; 118pp; English.  
XX

CC The present invention describes genetically modified cells (A) containing  
CC a polynucleotide (I) that encodes a polypeptide with heparanase activity,  
CC and express recombinant heparanase (II). Heparanase cleaves heparan  
CC sulphate (HS) at specific intrachain sites, resulting in release of  
CC heparin-binding growth factors, enzymes and proteins that are sequestered  
CC by HS in basement membranes, extracellular matrix or cell surfaces. It  
CC may also be implicated in tumour angiogenesis and metastases. (II) is  
CC potentially useful in wound healing and for treating angiogenesis,  
CC restenosis, atherosclerosis, inflammation, neurodegeneration, viral  
CC infection and cystic fibrosis. It can also be used to neutralise heparin  
CC (an alternative to protamine) and to screen for specific inhibitors  
CC (potentially useful for treating cancer and metastases). Antibodies  
CC raised against (II) are used for immunodetection and diagnosis of  
CC micrometastases, autoimmune lesions and kidney failure. (A) provide (II)  
CC in large quantities, in a form that is homogeneously processed and  
CC activated/neutralised by a dedicated protease. The present sequence  
CC represents human heparanase  
XX

SQ Sequence 543 AA;

Query Match 100.0%; Score 2842; DB 3; Length 543;  
Best Local Similarity 100.0%; Pred. No. 2.9e-273;  
Matches 543; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLLRSKPALPPPLMLLLGPGPLSPGALPPAQADVVLDFFTOEPLHLVSPSFLSVT 60  
Db 1 MLLRSKPALPPPLMLLLGPGPLSPGALPPAQADVVLDFFTOEPLHLVSPSFLSVT 60  
Qy 61 IDANLATDPRFLILLGSPKLTARGLSPAYLRFGGKTDFLIIDPKKESFEERSYQWS 120  
Db 61 IDANLATDPRFLILLGSPKLTARGLSPAYLRFGGKTDFLIIDPKKESFEERSYQWS 120  
Qy 121 QVNQDICKYGIIPPDVEEKLREWPYQQLLREHYQKKFNSTYSRSSVDVLYTFANC 180  
Db 121 QVNQDICKYGIIPPDVEEKLREWPYQQLLREHYQKKFNSTYSRSSVDVLYTFANC 180  
Qy 181 GLDLIFGLNALLRTADLOWNSSNAQLLLDYCSSKGYNISWELGNEPNSFLKADIFINGS 240  
Db 181 GLDLIFGLNALLRTADLOWNSSNAQLLLDYCSSKGYNISWELGNEPNSFLKADIFINGS 240  
Qy 241 QLGEDYIQLHKLKRSKTFKNAKLYGPDVGQPRRTAKMLKSLKAGGVIDSVTWHYYL 300  
Db 241 QLGEDYIQLHKLKRSKTFKNAKLYGPDVGQPRRTAKMLKSLKAGGVIDSVTWHYYL 300  
Qy 301 NGRTATREDFLNPVDLDFISSVQKVFQVVESTRPGKKVWLGETSSAYGGGAPLLSDTFA 360  
Db 301 NGRTATREDFLNPVDLDFISSVQKVFQVVESTRPGKKVWLGETSSAYGGGAPLLSDTFA 360



Db 301 NGRTATREDFLNPDVLDIFISSVQKVFQVVESTPRGKKWLGLETSSAYGGAPLLSDTFA 360  
 Qy 361 AGFMWLDKLGLSARMGIEVVMRQVFFGAGNYHLVDENFDPLPDYWL SLLFKKLVGTKVL 420  
 Db 361 AGFMWLDKLGLSARMGIEVVMRQVFFGAGNYHLVDENFDPLPDYWL SLLFKKLVGTKVL 420  
 Qy 421 ASVQGSRRRLRVYLHCTNTDNPYKEGDLTLAYAINLHNVTKYLR LPPYPSNKKQVDKYL 480  
 Db 421 ASVQGSRRRLRVYLHCTNTDNPYKEGDLTLAYAINLHNVTKYLR LPPYPSNKKQVDKYL 480  
 Qy 481 RPLGPHGLLSKSVQNLGTLKMWDDQTLPLMEKPLRPGSSGLG LPAFYSFFVIRNAKVA 540  
 Db 481 RPLGPHGLLSKSVQNLGTLKMWDDQTLPLMEKPLRPGSSGLG LPAFYSFFVIRNAKVA 540  
 Qy 541 ACI 543  
 Db 541 ACI 543  
 RESULT 3  
 AAB08849  
 ID AAB08849 standard; protein; 543 AA.  
 XX  
 AC AAB08849;  
 DT 15-JAN-2001 (first entry)  
 XX  
 DE Amino acid sequence of a human heparanase polypeptide.  
 XX  
 KW Human; heparanase; gene therapy; tumour; inflammation; autoimmunity;  
 KW heparin-binding growth factor; cytokine; neurodegenerative plaque;  
 KW wound healing; infection; burn; angiogenesis; restenosis;  
 KW atherosclerosis; inflammation; neurodegenerative disease;  
 KW Gerstmann-Straussler Syndrome; Creutzfeldt-Jakob disease.  
 XX  
 OS Homo sapiens.  
 XX  
 FN WO200052178-A1.  
 XX  
 PD 08-SEP-2000.  
 XX  
 PF 14-FEB-2000; 2000WO-US003542.  
 XX  
 PR 01-MAR-1999; 99US-00258892.  
 XX  
 PA (INSI-) INSIGHT STRATEGY & MARKETING LTD.  
 PA (HADA-) HADASIT MEDICAL RES SERVICES & DEV.  
 PA (FRIE/) FRIEDMAN M M.  
 XX  
 PI Pecker I, Vlodavsky I, Feinstein E;  
 XX  
 DR WPI; 2000-579289/54.  
 DR N-PSDB; AAAV5051.  
 XX  
 PT New polynucleotides encoding a polypeptide having heparanase activity,  
 useful in wound healing and in gene therapy, particularly in treating  
 tumor, inflammation, autoimmunity, neurodegenerative diseases.  
 XX  
 PS Claim 22; Fig 1; 152pp; English.  
 XX  
 CC The present sequence represents a human protein with heparanase catalytic  
 activity. The heparanase (hpa) polynucleotide is useful in gene therapy,  
 particularly in treating tumour, inflammation or autoimmunity.  
 CC Particularly, the polynucleotide is useful in modulating the  
 bioavailability of heparin-binding growth factors, cellular responses to  
 heparin-binding growth factors (e.g. bFGF) and cytokines (e.g.  
 interleukin (IL)-8), cell interaction with plasma lipoproteins, cellular  
 susceptibility to certain viral and some bacterial and protozoa  
 infections, or disintegration of neurodegenerative plaques. The  
 polynucleotide is also useful in wound healing (e.g. thermal, chemical or  
 radiation burns), and in the treatment of angiogenesis, restenosis,  
 atherosclerosis, inflammation, neurodegenerative diseases (Gerstmann-  
 Straussler Syndrome or Creutzfeldt-Jakob disease), and some viral,

CC bacterial or protozoa infections  
 XX  
 SQ Sequence 543 AA;  
 Query Match 100.0%; Score 2842; DB 3; Length 543;  
 Best Local Similarity 100.0%; Pred. No. 2.9e-273;  
 Matches 543; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 MLRSKPALPPPLMLLLGLPLSPGALPRPAQADVLDLDFFTQPLHLVSPSFLSVT 60  
 Db 1 MLRSKPALPPPLMLLLGLPLSPGALPRPAQADVLDLDFFTQPLHLVSPSFLSVT 60  
 Qy 61 IDANLATDPRFLILLGSPKRLTLARGLSPAYLRFGGTKTDLIFDPKKESTFEERSYQWS 120  
 Db 61 IDANLATDPRFLILLGSPKRLTLARGLSPAYLRFGGTKTDLIFDPKKESTFEERSYQWS 120  
 Qy 121 QVNQDICKYGSIPPDVEEKLRLWPYQEQILLREHYQKKFNSTYSRSSVDVLYTFANCS 180  
 Db 121 QVNQDICKYGSIPPDVEEKLRLWPYQEQILLREHYQKKFNSTYSRSSVDVLYTFANCS 180  
 Qy 181 GLDLIFGLNALLRTADLQWNSNAQLLDYCSSKGYNISWELGNENPSFLKKADIFINGS 240  
 Db 181 GLDLIFGLNALLRTADLQWNSNAQLLDYCSSKGYNISWELGNENPSFLKKADIFINGS 240  
 Qy 241 QLGEDYIQLHKLRLKSTFKNAKLYGPDVGQPRRKTAKMLKSF LKAGGEVIDSVTWHYYL 300  
 Db 241 QLGEDYIQLHKLRLKSTFKNAKLYGPDVGQPRRKTAKMLKSF LKAGGEVIDSVTWHYYL 300  
 Qy 301 NGRTATREDFLNPDVLDIFISSVQKVFQVVESTPRGKKWLGLETSSAYGGAPLLSDTFA 360  
 Db 301 NGRTATREDFLNPDVLDIFISSVQKVFQVVESTPRGKKWLGLETSSAYGGAPLLSDTFA 360  
 Qy 361 AGFMWLDKLGLSARMGIEVVMRQVFFGAGNYHLVDENFDPLPDYWL SLLFKKLVGTKVL 420  
 Db 361 AGFMWLDKLGLSARMGIEVVMRQVFFGAGNYHLVDENFDPLPDYWL SLLFKKLVGTKVL 420  
 Qy 421 ASVQGSRRRLRVYLHCTNTDNPYKEGDLTLAYAINLHNVTKYLR LPPYPSNKKQVDKYL 480  
 Db 421 ASVQGSRRRLRVYLHCTNTDNPYKEGDLTLAYAINLHNVTKYLR LPPYPSNKKQVDKYL 480  
 Qy 481 RPLGPHGLLSKSVQNLGTLKMWDDQTLPLMEKPLRPGSSGLG LPAFYSFFVIRNAKVA 540  
 Db 481 RPLGPHGLLSKSVQNLGTLKMWDDQTLPLMEKPLRPGSSGLG LPAFYSFFVIRNAKVA 540  
 Qy 541 ACI 543  
 Db 541 ACI 543  
 RESULT 4  
 AAY52990  
 ID AAY52990 standard; protein; 543 AA.  
 XX  
 AC AAY52990;  
 XX  
 DT 21-FEB-2000 (first entry)  
 XX  
 DE Human heparanase protein sequence.  
 XX  
 KW Human; heparanase; hpa; diagnosis; therapy; tumour; cytostatic;  
 KW antidiabetic; immunomodulatory; anti-inflammatory; nephrotropic;  
 KW metastasis; adenocarcinoma; squamous cell carcinoma; teratocarcinoma;  
 KW mesothelioma; melanoma; lymphoma; leukemia; cancer; sepsis; diabetes;  
 KW inflammation; haemorrhagic nephritis; nephrotic syndrome;  
 KW autoimmune disease; anticancer; kidney disease.  
 XX  
 OS Homo sapiens.  
 XX  
 FN WO9957153-A1.  
 XX  
 PD 11-NOV-1999.  
 XX  
 PF 29-APR-1999; 99WO-US009255.



Db 241 QLGEDYIQLHKLKSTFKNAKLYGPDVGQPRRTAKMLKFLKAGGVIDSVTHHYYL 300  
 Qy 301 NGRATREDFLNPDVLDIFISSVQKVFQVVESTPGKVKWLGESSAYGGGAPLLSDTFA 360  
 Db 301 NGRATREDFLNPDVLDIFISSVQKVFQVVESTPGKVKWLGESSAYGGGAPLLSDTFA 360  
 Qy 361 AGFMWLDKGLSARMGIEVVMRQVFFGAGNYHLVDENFDPLDYWLSLLFKKLVGTVKYM 420  
 Db 361 AGFMWLDKGLSARMGIEVVMRQVFFGAGNYHLVDENFDPLDYWLSLLFKKLVGTVKYM 420  
 Qy 421 ASVQSGKRRKRVYLHCTNTDNPRYKEGDLTYAINLHNVTYKYLRLPYPPFSNKQVDKYL 480  
 Db 421 ASVQSGKRRKRVYLHCTNTDNPRYKEGDLTYAINLHNVTYKYLRLPYPPFSNKQVDKYL 480  
 Qy 481 RPLGPHGLLSKSVQNLGLTLKMWDDQTLPLMEKPLRPGSSGLGPAFSYSEFVIRNAKVA 540  
 Db 481 RPLGPHGLLSKSVQNLGLTLKMWDDQTLPLMEKPLRPGSSGLGPAFSYSEFVIRNAKVA 540  
 Qy 541 ACI 543  
 Db 541 ACI 543

## RESULT 6

ID ABB07813  
 AC ABB07813 standard; protein; 543 AA.

DT 03-JUL-2002 (first entry)  
 DE Human heparanase sequence.  
 KW Heparanase; catalytic; cytostatic; antiviral; antibacterial; enzyme;  
 KW anti-protozoan; neuroprotective; heparin; human.  
 OS Homo sapiens.

Key Location/Qualifiers

FT Peptide 1..35  
 FT Protein /note= "signal peptide"  
 FT Protein /note= "mature protein"

US2002034810-A1.

21-MAR-2002.

16-AUG-2001; 2001US-00930218.

20-SEP-2000; 2000US-00666390.

(INSI-) INSIGHT STRATEGY & MARKETING LTD.

Goldshmidt O, Pecker I, Vlodavsky I, Michal I, Zcharia E;

WPI; 2002-338926/37.

Nucleic acid encoding avian and reptile heparanase polypeptide is useful  
 to treat various heparin-related disorders and the signal peptide is  
 useful in production of membrane-targeted or secreted recombinant  
 proteins.

Disclosure; Fig 1a; 39pp; English.

The invention relates to an isolated avian and reptile nucleic acid,  
 encoding a polypeptide with heparanase catalytic activity. The signal  
 peptide of the nucleic acid can be used to express membrane-associated or  
 secreted proteins in heterologous expression systems. The encoded  
 polypeptides can be used to prevent tumour angiogenesis, metastasis and  
 invasion, and to intervene with pathologies associated with impaired  
 heparin-binding growth factors, cellular responses to heparin-binding

CC growth factors and cytokines, cell interaction with plasma lipoproteins,  
 CC cellular susceptibility to viral, protozoa and bacterial infections or  
 CC disinfection of neurodegenerative plaques. The present sequence  
 CC represents a human heparanase protein sequence used in similarity studies  
 XX  
 SQ Sequence 543 AA;

Query Match 100.0%; Score 2842; DB 5; Length 543;  
 Best Local Similarity 100.0%; Pred. No. 2.9e-273;  
 Matches 543; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLRSKAPALPPPLMLLLGLPLSPGALPRPAQADVDLDFFTQBPFLHVSFSLSVT 60  
 Db 1 MLRSKAPALPPPLMLLLGLPLSPGALPRPAQADVDLDFFTQBPFLHVSFSLSVT 60  
 Qy 61 IDANLATDPRFLIILGSPKLTLAGLSPAYLRGGTKTDFLI FDPKKESTFEERSYQWS 120  
 Db 61 IDANLATDPRFLIILGSPKLTLAGLSPAYLRGGTKTDFLI FDPKKESTFEERSYQWS 120  
 Qy 121 QVNODICKYGSIPPDVEEKLRLWPYQEQLLLRHYOKKFNKSTYSRSSVDVLYTFANCS 180  
 Db 121 QVNODICKYGSIPPDVEEKLRLWPYQEQLLLRHYOKKFNKSTYSRSSVDVLYTFANCS 180  
 Qy 181 GLDLIFGLNALLRTADLQWNSNAQLLDYCSSKGYNISWELGNEPNSFLKADIFINGS 240  
 Db 181 GLDLIFGLNALLRTADLQWNSNAQLLDYCSSKGYNISWELGNEPNSFLKADIFINGS 240  
 Qy 241 QLGEDYIQLHKLKSTFKNAKLYGPDVGQPRRTAKMLKFLKAGGVIDSVTHHYYL 300  
 Db 241 QLGEDYIQLHKLKSTFKNAKLYGPDVGQPRRTAKMLKFLKAGGVIDSVTHHYYL 300  
 Qy 301 NGRATREDFLNPDVLDIFISSVQKVFQVVESTPGKVKWLGESSAYGGGAPLLSDTFA 360  
 Db 301 NGRATREDFLNPDVLDIFISSVQKVFQVVESTPGKVKWLGESSAYGGGAPLLSDTFA 360  
 Qy 361 AGFMWLDKGLSARMGIEVVMRQVFFGAGNYHLVDENFDPLDYWLSLLFKKLVGTVKYM 420  
 Db 361 AGFMWLDKGLSARMGIEVVMRQVFFGAGNYHLVDENFDPLDYWLSLLFKKLVGTVKYM 420  
 Qy 421 ASVQSGKRRKRVYLHCTNTDNPRYKEGDLTYAINLHNVTYKYLRLPYPPFSNKQVDKYL 480  
 Db 421 ASVQSGKRRKRVYLHCTNTDNPRYKEGDLTYAINLHNVTYKYLRLPYPPFSNKQVDKYL 480  
 Qy 481 RPLGPHGLLSKSVQNLGLTLKMWDDQTLPLMEKPLRPGSSGLGPAFSYSEFVIRNAKVA 540  
 Db 481 RPLGPHGLLSKSVQNLGLTLKMWDDQTLPLMEKPLRPGSSGLGPAFSYSEFVIRNAKVA 540  
 Qy 541 ACI 543  
 Db 541 ACI 543

## RESULT 7

ID ADG88800  
 AC ADG88800 standard; protein; 543 AA.

11-MAR-2004 (first entry)

Human hpa protein.

Wound healing; heparanase; ulcer; burn; laceration; surgical incision;  
 necrosis; pressure wound; diabetic ulcer; angiogenesis; human; therapy.

Homo sapiens.

US2003161823-A1.

28-AUG-2003.

14-JAN-2003; 2003US-00341582.

```
PR 31-AUG-1998; 98WO-US017954.
PR 01-MAR-1999; 99US-00258892.
PR 06-FEB-2001; 2001US-00776874.
PR 05-SEP-2001; 2001WO-IL000830.
PR 19-NOV-2001; 2001US-00988113.
XX
PA (ILAN/) ILAN N.
PA (VLOD/) VLODAVSKY I.
PA (YACO/) YACOBY-ZEEVI O.
PA (PECK/) PECKER I.
PA (FEIN/) FEINSTEIN E.
XX
PI Ilan N, Vlodavsky I, Yacoby-Zeevi O, Pecker I, Feinstein E;
XX
XX WPI; 2003-897910/82.
DR N-PSDB; ADG88799, ADG88801, ADG88832.
XX
XX Composition for treating a wound comprising recombinant heparanase is
PT useful to induce or accelerate wound healing and induce or accelerate
PT angiogenesis.
XX
XX Claim 2; SEQ ID NO 10; 143pp; English.
XX
XX The present invention relates to methods and compositions for inducing
CC and/or accelerating wound healing via the catalytic activity of
CC heparanase. The invention is used to induce or accelerate a healing
CC process, particularly of an ulcer, burn, laceration, surgical incision,
CC necrosis, pressure wound, diabetic ulcer and to induce or accelerate
CC angiogenesis. The present sequence is human hpa protein.
XX
XX Sequence 543 AA;
SQ
Query Match 100.0%; Score 2842; DB 7; Length 543;
Best Local Similarity 100.0%; Pred. No. 2.9e-273;
Matches 543; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MLLRSKPALPPLMLLLGPGSPGALPPAQADVVLDFFTOEPLHLVSPFLSVT 60
Db 1 MLLRSKPALPPLMLLLGPGSPGALPPAQADVVLDFFTOEPLHLVSPFLSVT 60
Qy 61 IDANLATDPRFLILGSPKLTARGLSPAYLRFGGTKTDFLIFPKKESFEERSYQWS 120
Db 61 IDANLATDPRFLILGSPKLTARGLSPAYLRFGGTKTDFLIFPKKESFEERSYQWS 120
Qy 121 QVNQDICKYGSIPDPVEEKLREWPYQQLLREHYQKKFNSTYSRSSVDLYTFANCS 180
Db 121 QVNQDICKYGSIPDPVEEKLREWPYQQLLREHYQKKFNSTYSRSSVDLYTFANCS 180
Qy 181 GLDLIFGNALLRTADLQWSSNAQLLLDYCSSKGYNISWELGNEPNSFLKKADIFINGS 240
Db 181 GLDLIFGNALLRTADLQWSSNAQLLLDYCSSKGYNISWELGNEPNSFLKKADIFINGS 240
Qy 241 QLGEDIYQLHKLRLKSTFNKAKLYGPDVGQPRRKTKAKMLKSPFKAGGVIDSVTWHHYLL 300
Db 241 QLGEDIYQLHKLRLKSTFNKAKLYGPDVGQPRRKTKAKMLKSPFKAGGVIDSVTWHHYLL 300
Qy 301 NGRTRATREDFLNPVDLIFISVQVKVQFVQVSTREPCKKWLGETSSAYGGAPLLSDTFA 360
Db 301 NGRTRATREDFLNPVDLIFISVQVKVQFVQVSTREPCKKWLGETSSAYGGAPLLSDTFA 360
Qy 361 AGFWMLDKLGLSARMGIEVWVRQVFFGAGNVHLVDENFDPLDYWLSLFLFKLVGTVKVL 420
Db 361 AGFWMLDKLGLSARMGIEVWVRQVFFGAGNVHLVDENFDPLDYWLSLFLFKLVGTVKVL 420
Qy 421 ASVQGSKRRKRLVYLHCTNTDNPRYKEGDLTLAYLNHNVTYKLRPLPYFNSKNQVDKYL 480
Db 421 ASVQGSKRRKRLVYLHCTNTDNPRYKEGDLTLAYLNHNVTYKLRPLPYFNSKNQVDKYL 480
Qy 481 RPLGPHGLLSKSVQVNLGTLKMWDDQTLPLMEKPLRPGSSIGLPAFYSFPIRNAKVA 540
Db 481 RPLGPHGLLSKSVQVNLGTLKMWDDQTLPLMEKPLRPGSSIGLPAFYSFPIRNAKVA 540
Qy 541 ACI 543
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Db 541 ACI 543
|||
ADL16379 standard; protein; 543 AA.
XX
AC ADL16379;
XX
DT 06-MAY-2004 (first entry)
XX
DE Human heparanase partial protein.
XX
XX Human; heparanase; heparanase-dependent cancer; cancer;
KW autoimmune reaction; inflammation; chromosome 4; enzyme.
XX
OS Homo sapiens.
XX
PN US2003236215-A1.
XX
PD 25-DEC-2003.
XX
XX 09-JUN-2003; 2003US-00456573.
XX
XX 31-AUG-1998; 98WO-US017954.
XX
XX 01-MAR-1999; 99US-00258892.
XX
XX 08-NOV-1999; 99US-00435739.
XX
XX (INSI-) INSIGHT STRATEGY & MARKETING LTD.
XX
XX (HADA-) HADASIT MEDICAL RES SERVICES & DEV.
XX
XX Pecker I, Vlodavsky I, Feinstein E;
XX
XX WPI; 2004-070610/07.
XX
XX New antisense oligonucleotide hybridizable with a polynucleotide encoding
PT a polypeptide with heparanase activity, useful for treating diseases such
PT as cancer and autoimmune disorders.
XX
XX Claim 3; SEQ ID NO 10; 108pp; English.
XX
XX The invention relates to an antisense oligonucleotide (ASO) comprising a
CC polynucleotide or a polynucleotide analogue of at least 10 bases being
CC hybridisable in vivo, under physiological conditions, with a portion of
CC a polynucleotide strand encoding a polypeptide having heparanase
CC catalytic activity. Also included are a method of in vivo downregulating
CC heparanase activity (comprising administering the ASO in vivo), a method
CC of treating a subject suffering from a pathological condition
CC (characterised by heparanase activity, comprising administering ASO to
CC the subject), a pharmaceutical composition comprising the ASO and a
CC carrier, an antisense nucleic acid construct (comprising a promoter
CC sequence and a polynucleotide sequence directing the synthesis of an
CC antisense RNA sequence of at least 10 bases being hybridisable in vivo,
CC under physiological conditions, with a polynucleotide strand encoding a
CC polypeptide having heparanase catalytic activity), a method of in vivo
CC downregulating heparanase activity (comprising administering in vivo the
CC antisense nucleic acid construct), a pharmaceutical composition
CC comprising the antisense nucleic acid construct and a carrier, and an
CC analogue of at least 10 bases being hybridisable in vivo, under
CC physiological conditions, with a portion of a polynucleotide strand being
CC characterised by forming at least a portion of an untranslated region
CC (UTR) for a polynucleotide strand encoding a polypeptide having
CC heparanase catalytic activity. The methods and compositions of the
CC present invention are useful for the prevention and/or treatment of
CC diseases or conditions associated with aberrant heparanase activity, such
CC as heparanase-dependent cancer, cancer, autoimmune reaction and
CC inflammation. The gene for human heparanase is located on chromosome 4.
XX The present sequence is a human heparanase protein.
XX Sequence 543 AA;
```

Query Match 100.0%; Score 2842; DB 8; Length 543;  
Best Local Similarity 100.0%; Pred. No. 2.9e-273;  
Matches 543; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLLRSKALPPPLMLLLGPGPLSPGALPRPAQADVDLDFDTQPLHLVSPFLSVT 60  
Db 1 MLLRSKALPPPLMLLLGPGPLSPGALPRPAQADVDLDFDTQPLHLVSPFLSVT 60

Qy 61 IDANLATDPRFLIILGSPKLTLAGLSPAYLRFGGKTDFLIPDPKKESTFEERSYQWS 120  
Db 61 IDANLATDPRFLIILGSPKLTLAGLSPAYLRFGGKTDFLIPDPKKESTFEERSYQWS 120

Qy 121 QVNQDICKYGSIPDPVEEKLRLWPYQEQLLLRHYOKKFNSTYSRSSVDVLYTFANCS 180  
Db 121 QVNQDICKYGSIPDPVEEKLRLWPYQEQLLLRHYOKKFNSTYSRSSVDVLYTFANCS 180

Qy 181 GLDLIFGLNALLRTADLQWSSNAQLLLDYCSSKGYNISWELGNEPNSFLKKADIFINGS 240  
Db 181 GLDLIFGLNALLRTADLQWSSNAQLLLDYCSSKGYNISWELGNEPNSFLKKADIFINGS 240

Qy 241 QLGEDYIQLHKLRLKSTFKNAKLYGPDVGQPRRTAKMLKSFLKAGGEVIDSVTWHYYL 300  
Db 241 QLGEDYIQLHKLRLKSTFKNAKLYGPDVGQPRRTAKMLKSFLKAGGEVIDSVTWHYYL 300

Qy 301 NGRTATREDFLNPVDLIDIFISSVQKVFQVVESTPRGKKWILGETSSAYGGAPLLSDTFA 360  
Db 301 NGRTATREDFLNPVDLIDIFISSVQKVFQVVESTPRGKKWILGETSSAYGGAPLLSDTFA 360

Qy 361 AGFMWLDKLGLSARMGIEVVMRQVFFGAGNYHLVDENFDPLPDYWLISLLFKLGVTKVLM 420  
Db 361 AGFMWLDKLGLSARMGIEVVMRQVFFGAGNYHLVDENFDPLPDYWLISLLFKLGVTKVLM 420

Qy 421 ASVQGSRRKRLRVYLHCTNTDNPYKEGDLTLVAINLHNVTKYLRPLPFSNKKQVDKYL 480  
Db 421 ASVQGSRRKRLRVYLHCTNTDNPYKEGDLTLVAINLHNVTKYLRPLPFSNKKQVDKYL 480

Qy 481 RPLGPHGLLSKSVQLNGLTLKWVDDQTLPLPMEKPLPGSSSLGLPAPFSYFFVIRNAKVA 540  
Db 481 RPLGPHGLLSKSVQLNGLTLKWVDDQTLPLPMEKPLPGSSSLGLPAPFSYFFVIRNAKVA 540

RESULT 9  
ADM48716  
ID ADM48716 standard; protein; 543 AA.

AC ADM48716;  
XX 03-JUN-2004 (first entry)  
XX Human hpa protein #1.  
XX Transgenic animal; heparanase; cancer; viral infection; restenosis;  
XX neurodegenerative disease; atherosclerosis; pulmonary disorder; hpa;  
XX human.  
XX Homo sapiens.  
XX US2003217375-A1.  
XX 20-NOV-2003.  
XX 24-FEB-2003; 2003US-00371218.  
XX 31-AUG-1998; 98WO-US017954.  
XX 01-MAR-1999; 99US-00258892.  
XX 06-FEB-2001; 2001US-00776874.  
XX 19-NOV-2001; 2001US-00988113.  
XX (ZCHA/) ZCHARIA E.

(VLOD/) VLODAVSKY I.  
(METZ/) METZGER S.  
(PECK/) PECKER I.  
(ILAN/) ILAN N.  
(CHAJ/) CHAJEK-SHAUL T.  
(GOLD/) GOLDSHMIDT O.  
XX Zcharia E, Vlodavsky I, Metzger S, Pecker I, Ilan N;  
PI Chajek-Shaul T, Goldshmidt O;  
XX WPI: 2004-021918/02.  
DR N-PSDB; ADM48715, ADM48717.  
XX New transgenic non-human animal expressing heparinase, useful as models  
PT for human disease, such as cancers, viral infection, neurodegenerative  
PT diseases, restenosis, atherosclerosis and pulmonary disorders.  
XX Example 1; SEQ ID NO 10; 106pp; English.  
XX The present invention relates to a transgenic non-human animal whose  
CC genome comprises an exogenous polynucleotide sequence, including a  
CC promoter active in tissues of the non-human, a region encoding a human  
CC heparanase, where the promoter and the region encoding human heparanase  
CC are operably linked in the exogenous polynucleotide such that human  
CC heparanase is expressed in at least a portion of the cells of the non-  
CC human animal. The methods and compositions of the present invention are  
CC useful for the production of transgenic animals expressing heparanase, to  
CC be used as models for human diseases such as cancers, viral infection,  
CC restenosis, neurodegenerative diseases, atherosclerosis and pulmonary  
CC disorders. The present sequence is human hpa protein used in the  
CC exemplification of the invention.  
XX SQ Sequence 543 AA;  
Query Match 100.0%; Score 2842; DB 8; Length 543;  
Best Local Similarity 100.0%; Pred. No. 2.9e-273;  
Matches 543; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLLRSKALPPPLMLLLGPGPLSPGALPRPAQADVDLDFDTQPLHLVSPFLSVT 60  
Db 1 MLLRSKALPPPLMLLLGPGPLSPGALPRPAQADVDLDFDTQPLHLVSPFLSVT 60

Qy 61 IDANLATDPRFLIILGSPKLTLAGLSPAYLRFGGKTDFLIPDPKKESTFEERSYQWS 120  
Db 61 IDANLATDPRFLIILGSPKLTLAGLSPAYLRFGGKTDFLIPDPKKESTFEERSYQWS 120

Qy 121 QVNQDICKYGSIPDPVEEKLRLWPYQEQLLLRHYOKKFNSTYSRSSVDVLYTFANCS 180  
Db 121 QVNQDICKYGSIPDPVEEKLRLWPYQEQLLLRHYOKKFNSTYSRSSVDVLYTFANCS 180

Qy 181 GLDLIFGLNALLRTADLQWSSNAQLLLDYCSSKGYNISWELGNEPNSFLKKADIFINGS 240  
Db 181 GLDLIFGLNALLRTADLQWSSNAQLLLDYCSSKGYNISWELGNEPNSFLKKADIFINGS 240

Qy 241 QLGEDYIQLHKLRLKSTFKNAKLYGPDVGQPRRTAKMLKSFLKAGGEVIDSVTWHYYL 300  
Db 241 QLGEDYIQLHKLRLKSTFKNAKLYGPDVGQPRRTAKMLKSFLKAGGEVIDSVTWHYYL 300

Qy 301 NGRTATREDFLNPVDLIDIFISSVQKVFQVVESTPRGKKWILGETSSAYGGAPLLSDTFA 360  
Db 301 NGRTATREDFLNPVDLIDIFISSVQKVFQVVESTPRGKKWILGETSSAYGGAPLLSDTFA 360

Qy 361 AGFMWLDKLGLSARMGIEVVMRQVFFGAGNYHLVDENFDPLPDYWLISLLFKLGVTKVLM 420  
Db 361 AGFMWLDKLGLSARMGIEVVMRQVFFGAGNYHLVDENFDPLPDYWLISLLFKLGVTKVLM 420

Qy 421 ASVQGSRRKRLRVYLHCTNTDNPYKEGDLTLVAINLHNVTKYLRPLPFSNKKQVDKYL 480  
Db 421 ASVQGSRRKRLRVYLHCTNTDNPYKEGDLTLVAINLHNVTKYLRPLPFSNKKQVDKYL 480

Qy 481 RPLGPHGLLSKSVQLNGLTLKWVDDQTLPLPMEKPLPGSSSLGLPAPFSYFFVIRNAKVA 540  
Db 481 RPLGPHGLLSKSVQLNGLTLKWVDDQTLPLPMEKPLPGSSSLGLPAPFSYFFVIRNAKVA 540

QY 541 ACI 543  
 DB 541 ACI 543

RESULT 10  
 AEA42466  
 ID AEA42466 standard; protein; 543 AA.  
 XX AC AEA42466;  
 XX 28-JUL-2005 (first entry)  
 DT Human heparanase protein.  
 DE antibody; heparanase; antiinflammatory; vulnery; immunosuppressive;  
 KW antiangiogenic; cytostatic; antiarteriosclerotic; vasotropic;  
 KW inflammation; wound healing; scarring; vasculopathy; autoimmune disease;  
 KW angiogenesis disorder; cancer; tumor; metastasis.  
 XX Homo sapiens.  
 OS AU2004201462-A1.  
 PN 06-MAY-2004.  
 PD 08-APR-2004; 2004AU-00201462.  
 PF 08-APR-2004; 2004AU-00201462.  
 PR (INSI-) INSIGHT BIOPHARMACEUTICALS LTD.  
 XX (HADA-) HADASTI MEDICAL RES SERVICES & DEV LTD.  
 PA Vlodavsky I, Pecker I, Miron M, Gilboa A, Miron D, Moskowitz H;  
 PI Shlomi Y, Peleg Y, Yacoby-Zeevi O, Ayal-Hershkovitz M, Ben-Artzi H;  
 PI Feinstein E;  
 XX WPI; 2005-173343/19.  
 DR N-PSDB; AEA42465, AEA42434, AEA42435.  
 XX Novel isolated antibody capable of specifically binding to epitope of  
 PT heparanase protein, useful for preventing and treating heparanase-related  
 PT disorder such as inflammatory disorder, scars, autoimmune conditions or  
 PT angiogenesis.  
 XX Example 8; Fig 47; 260pp; English.

The invention relates to an isolated antibody or its portion (I) capable  
 of specifically binding to an epitope of a heparanase protein. Also  
 described: (1) a cell line (II) for producing a monoclonal antibody or  
 its portion, comprising a cell line for producing (I); (2) a  
 pharmaceutical composition comprising (I) and a carrier; and (3) an  
 affinity medium (III) for binding human heparanase polypeptides,  
 comprising (I) immobilized to a chemically inert, insoluble carrier. (I)  
 useful for treating a subject suffering from a pathological condition,  
 which involves administering (I) to the subject. (I) is useful for  
 preventing and treating heparanase-related disorder or condition chosen  
 from inflammatory disorder, wound, scar, vasculopathy, autoimmune  
 condition, angiogenesis, cell proliferation, cancerous condition, tumor  
 cell proliferation, invasion of circulating tumor cells and metastatic  
 disease. (I) is useful for detecting the presence of heparanase  
 polypeptide in a sample. (I) is useful for detecting heparanase-related  
 disease or condition in a subject such as vertebrate, preferably mammal  
 e.g., human. The heparanase-related disorder or condition further  
 includes renal disease or disorder chosen from diabetic nephropathy,  
 glomerulosclerosis, nephrotic syndrome, minimal change nephrotic syndrome  
 and renal cell carcinoma. The present sequence represents human  
 heparanase, which is used in the exemplification of the present  
 invention.

Sequence 543 AA;

Query Match 100.0%; Score 2842; DB 9; Length 543;  
 Best Local Similarity 100.0%; Pred. No. 2.9e-273;  
 Matches 543; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLRSKDALPPPLMLLLGPGPLSPGALPRPAQAQDVVDLDFPTQBPPLHLVSPSFLSVT 60  
 DB 1 MLLRSKDALPPPLMLLLGPGPLSPGALPRPAQAQDVVDLDFPTQBPPLHLVSPSFLSVT 60

QY 61 IDANLATDPRFLIILGSPKLTARGLSPAYLRGGTKTDLIFDPKKESTFEERSYWQS 120  
 DB 61 IDANLATDPRFLIILGSPKLTARGLSPAYLRGGTKTDLIFDPKKESTFEERSYWQS 120

QY 121 QVNODICKYGSIPPDVEEKLRLWPYQQLLLRHHYQKFKNSTYSRSSVDVLYTFANC 180  
 DB 121 QVNODICKYGSIPPDVEEKLRLWPYQQLLLRHHYQKFKNSTYSRSSVDVLYTFANC 180

QY 181 GLDLIFGLNALLRTADLQWSSNAQLLLDYCSSKGYNISWELGNPNPSFLKKADIFINGS 240  
 DB 181 GLDLIFGLNALLRTADLQWSSNAQLLLDYCSSKGYNISWELGNPNPSFLKKADIFINGS 240

QY 241 QLGEDYIQLHKLRLKSTFKNAKLYGPDVGQPRRTAKMLKSLFKAGGEVIDSVTWHHYL 300  
 DB 241 QLGEDYIQLHKLRLKSTFKNAKLYGPDVGQPRRTAKMLKSLFKAGGEVIDSVTWHHYL 300

QY 301 NGRTATREDFLNPDVLDIFISSVOKVFQVVESTTRPGKKVWLGETSSAYGGAPLLSDTFA 360  
 DB 301 NGRTATREDFLNPDVLDIFISSVOKVFQVVESTTRPGKKVWLGETSSAYGGAPLLSDTFA 360

QY 361 AGFMWLDKLGSLARMGIEVVMRQVFFGAGNHYLVDENFDPPLPDYWLISLLFKKLVGTQVLM 420  
 DB 361 AGFMWLDKLGSLARMGIEVVMRQVFFGAGNHYLVDENFDPPLPDYWLISLLFKKLVGTQVLM 420

QY 421 ASVQGSRRKRLRVYLHCTNTDNPRYKSGDLTLIYAINLHNVTYLRLLPYPPSNKQVDKYL 480  
 DB 421 ASVQGSRRKRLRVYLHCTNTDNPRYKSGDLTLIYAINLHNVTYLRLLPYPPSNKQVDKYL 480

QY 481 RPLGPHGLLSKSVQLNGLTLKQVDDQTLPLMEKPLRPGSSGLPFAFSYSFFVI RNAKVA 540  
 DB 481 RPLGPHGLLSKSVQLNGLTLKQVDDQTLPLMEKPLRPGSSGLPFAFSYSFFVI RNAKVA 540

QY 541 ACI 543  
 DB 541 ACI 543

RESULT 11  
 AAY02346  
 ID AAY02346 standard; protein; 592 AA.  
 XX AC AAY02346;  
 XX 09-JUL-1999 (first entry)  
 DT A human heparanase protein.  
 DE Heparanase; hpa; modulator; heparin-binding growth factor;  
 KW cellular response; cytokine; cell interaction; plasma lipoprotein;  
 KW cellular susceptibility; infection; disintegration;  
 KW neurodegenerative plaque; wound healing; angiogenesis; restenosis;  
 KW atherosclerosis; inflammation; neurodegenerative disease; neutralise;  
 KW plasma heparin; micrometastasis; autoimmune lesion; renal failure.  
 XX Homo sapiens.  
 OS WO9911798-A1.  
 PN 11-MAR-1999.  
 PD 31-AUG-1998; 98WO-US017954.  
 PF 02-SEP-1997; 97US-00922170.  
 PR 02-JUL-1998; 98US-00109386.  
 XX

PA (INSI-) INSIGHT STRATEGY & MARKETING LTD.  
PA (HADA-) HADASIT MEDICAL. RES SERVICES & DEV.  
PA (FRIE/) FRIEDMAN M M.

PI Pecker I, Vladavsky I, Feinstein E;

DR WPI; 1999-302255/25.

XX	New human polynucleotide useful for treating angiogenesis, restenosis, and inflammation.
PT	
PT	
DK	
N-PSDB; AAX35650.	

PS Claim 6; Page 65-66; 63pp; English.

The specification describes a polypeptide having heparanase (hpa) activity. The recombinant protein is used as a modulator of heparin-binding growth factors, cellular responses to heparin-binding growth factors and cytokines, cell interaction with plasma lipoproteins, cellular susceptibility to viral, protozoal and bacterial infections or disintegration of neurodegenerative plaques. Heparanase may be useful for conditions such as wound healing, angiogenesis, restenosis, atherosclerosis, inflammation, neurodegenerative diseases, and viral infections. Mammalian heparanase can be used to neutralize plasma heparin, and anti-heparanase antibodies may be applied for immunodetection and diagnosis of micrometastases, autoimmune lesions, and renal failure in biopsy specimens, plasma samples, and body fluids. The present sequence represents human heparanase

Sequence 592 AA;

RESULT 12

AAB08850

ID AAB08850 standard; protein; 592 AA.

AA AAB08850;

15-JAN-2001 (first entry)

DE Amino acid sequence of a human heparanase polypeptide.

Human; heparanase; gene therapy; tumour; inflammation; autoimmunity;  
 heparin-binding growth factor; cytokine; neurodegenerative plaque;  
 wound healing; infection; burn; angiogenesis; restenosis;  
 atherosclerosis; inflammation; neurodegenerative disease;  
 Gerstmann-Sträussler Syndrome; Creutzfeldt-Jakob disease.

OS Homo sapiens.

PN WO200052178-A1.

08-SEP-2000

14-FEB-2000: 2000WO-IIS003542-XX  
PEXX  
PR 01-MAR-1999: 99US-00258892.

XX (PA) (INSI-) INSIGHT STRATEGY & MARKETING LTD.  
PA (HADA-) HADASIT MEDICAL RES SERVICES & DEV.  
PA (FRIE/) FRIEDMAN M M.

PI pecker I, Vlodysky I, Feinstein E:

WPI: 2000-579289/54.

DR N-PSDB; AAA75053.

New polynucleotides encoding a polypeptide having heparanase activity useful in wound healing and in gene therapy, particularly in treating tumor, inflammation, autoimmunity, neurodegenerative diseases.

PS Claim 22; Page 122-123; 152pp; English.

The present sequence represents a human protein with heparanase catalytic activity. The heparanase (hpa) polynucleotide is useful in gene therapy, particularly in treating tumour, inflammation or autoimmunity. Particularly, the polynucleotide is useful in modulating the bioavailability of heparin-binding growth factors, cellular responses to heparin-binding growth factors (e.g. bFGF) and cytokines (e.g. interleukin (IL)-8), cell interaction with plasma lipoproteins, cellular susceptibility to certain viral and some bacterial and protozoa infections, or disintegration of neurodegenerative plaques. The polynucleotide is also useful in wound healing (e.g. thermal, chemical or radiation burns), and in the treatment of angiogenesis, restenosis, atherosclerosis, inflammation, neurodegenerative diseases (Gerstmann-Sträussler Syndrome or Creutzfeldt-Jakob disease), and some viral, bacterial or protozoa infections.

Sequence 592 AA:

Db 170 QVNQDICKYGIIPDPVEKLRLEWYQEQLLREHYQKKFNSTYSRSSVDVLYTFANCS 229  
Qy 181 GLDLIFGLNALLRTADLQWNSNAQLLLDYCSSKGYNISWELGNEPNSFLKKADIFINGS 240  
Db 230 GLDLIFGLNALLRTADLQWNSNAQLLLDYCSSKGYNISWELGNEPNSFLKKADIFINGS 289  
Qy 241 QLGEDYIQLHKLKLRKSTFKNAKLYGPDVGQPRRTAKMLKSFLLKAGGEVIDSVTWHYYL 300  
Db 290 QLGEDYIQLHKLKLRKSTFKNAKLYGPDVGQPRRTAKMLKSFLLKAGGEVIDSVTWHYYL 349  
Qy 301 NGRTATREDFLNPDVLDIFISSVQKVFQVVESTREPKKVMWLGESAYGGAPLLSDTFA 360  
Db 350 NGRTATREDFLNPDVLDIFISSVQKVFQVVESTREPKKVMWLGESAYGGAPLLSDTFA 409  
Qy 361 AGFWMLDKGLSARMGIEVVMRQVFFGAGNYHLVDENFDPLPDYWLSSLFLLKLVGTKVLM 420  
Db 410 AGFWMLDKGLSARMGIEVVMRQVFFGAGNYHLVDENFDPLPDYWLSSLFLLKLVGTKVLM 469  
Qy 421 ASVOGSKRRKLRVYLHCTNTDNPRYKGGDLTYAINLHNVTKYLRLPYFFSNKQVDKYL 480  
Db 470 ASVOGSKRRKLRVYLHCTNTDNPRYKGGDLTYAINLHNVTKYLRLPYFFSNKQVDKYL 529  
Qy 481 RPLGPHGLLSKSVQLNGLTLLKQVDDQTLPLMEKPLRPGSSGLGPAFYSYSPFVIRNAKVA 540  
Db 530 RPLGPHGLLSKSVQLNGLTLLKQVDDQTLPLMEKPLRPGSSGLGPAFYSYSPFVIRNAKVA 589  
Qy 541 ACI 543  
Db 590 ACI 592

RESULT 13  
ADG88804  
ID ADG88804 standard; protein; 592 AA.  
XX AC ADG88804;  
XX DT 11-MAR-2004 (first entry)  
XX DE Human SK-hep1 protein.  
XX KW Wound healing; heparanase; ulcer; burn; laceration; surgical incision;  
XX KW necrosis; pressure wound; diabetic ulcer; angiogenesis; human; therapy.  
XX OS Homo sapiens.  
XX PN US2003161823-A1.  
XX PD 28-AUG-2003.  
XX PF 14-JAN-2003; 2003US-00341582.  
XX PR 31-AUG-1998; 98WO-US017954.  
XX PR 01-MAR-1999; 99US-00258892.  
XX PR 06-FEB-2001; 2001US-00776874.  
XX PR 05-SEP-2001; 2001WO-IL000830.  
XX PR 19-NOV-2001; 2001US-00988113.  
XX PA (ILAN/) ILAN N.  
XX PA (VLQD/) VLQDASKY I.  
XX PA (YACO/) YACOBY-ZEEVI O.  
XX PA (PECK/) PECKER I.  
XX PA (FEIN/) FEINSTEIN E.  
XX PI Ilan N, Vlodavsky I, Yacoby-Zeevi O, Pecker I, Feinstein E;  
XX WPI; 2003-897910/82.  
XX DR N-PSDB; ADG88803, ADG88805.  
XX PT Composition for treating a wound comprising recombinant heparanase is  
XX PT useful to induce or accelerate wound healing and induce or accelerate  
XX PT angiogenesis.

XX PS Claim 2; SEQ ID NO 14; 143pp; English.  
XX CC The present invention relates to methods and compositions for inducing  
CC and/or accelerating wound healing via the catalytic activity of  
CC heparanase. The invention is used to induce or accelerate a healing  
CC process, particularly of an ulcer, burn, laceration, surgical incision,  
CC necrosis, pressure wound, diabetic ulcer and to induce or accelerate  
CC angiogenesis. The present sequence is human SK-hep1 protein.  
XX SQ Sequence 592 AA;  
Query Match 100.0%; Score 2842; DB 7; Length 592;  
Best Local Similarity 100.0%; Pred. No. 3.3e-273; Indels 0; Gaps 0;  
Matches 543; Conservative 0; Mismatches 0;  
Qy 1 MLLRSKAPALPPPLMLLLGLPLSPGALPRPAQAQDVVDLDFFTQEPHLVSPSFLSVT 60  
Db 50 MLLRSKAPALPPPLMLLLGLPLSPGALPRPAQAQDVVDLDFFTQEPHLVSPSFLSVT 109  
Qy 61 IDANLATDPRPLILLGSPKLTLAGLSPAYLRFGTKTDFLIIDPKKESTFEERSYQWS 120  
Db 110 IDANLATDPRPLILLGSPKLTLAGLSPAYLRFGTKTDFLIIDPKKESTFEERSYQWS 169  
Qy 121 QVNODICKYGIIPDPVEKLRLEWYQEQLLREHYQKKFNSTYSRSSVDVLYTFANCS 180  
Db 170 QVNODICKYGIIPDPVEKLRLEWYQEQLLREHYQKKFNSTYSRSSVDVLYTFANCS 229  
Qy 181 GLDLIFGLNALLRTADLQWNSNAQLLLDYCSSKGYNISWELGNEPNSFLKKADIFINGS 240  
Db 230 GLDLIFGLNALLRTADLQWNSNAQLLLDYCSSKGYNISWELGNEPNSFLKKADIFINGS 289  
Qy 241 QLGEDYIQLHKLKLRKSTFKNAKLYGPDVGQPRRTAKMLKSFLLKAGGEVIDSVTWHYYL 300  
Db 290 QLGEDYIQLHKLKLRKSTFKNAKLYGPDVGQPRRTAKMLKSFLLKAGGEVIDSVTWHYYL 349  
Qy 301 NGRTATREDFLNPDVLDIFISSVQKVFQVVESTREPKKVMWLGESAYGGAPLLSDTFA 360  
Db 350 NGRTATREDFLNPDVLDIFISSVQKVFQVVESTREPKKVMWLGESAYGGAPLLSDTFA 409  
Qy 361 AGFWMLDKGLSARMGIEVVMRQVFFGAGNYHLVDENFDPLPDYWLSSLFLLKLVGTKVLM 420  
Db 410 AGFWMLDKGLSARMGIEVVMRQVFFGAGNYHLVDENFDPLPDYWLSSLFLLKLVGTKVLM 469  
Qy 421 ASVOGSKRRKLRVYLHCTNTDNPRYKGGDLTYAINLHNVTKYLRLPYFFSNKQVDKYL 480  
Db 470 ASVOGSKRRKLRVYLHCTNTDNPRYKGGDLTYAINLHNVTKYLRLPYFFSNKQVDKYL 529  
Qy 481 RPLGPHGLLSKSVQLNGLTLLKQVDDQTLPLMEKPLRPGSSGLGPAFYSYSPFVIRNAKVA 540  
Db 530 RPLGPHGLLSKSVQLNGLTLLKQVDDQTLPLMEKPLRPGSSGLGPAFYSYSPFVIRNAKVA 589  
Qy 541 ACI 543  
Db 590 ACI 592  
RESULT 14  
ADL16383  
ID ADL16383 standard; protein; 592 AA.  
XX AC ADL16383;  
XX DT 06-MAY-2004 (first entry)  
XX DE Human heparanase full length protein.  
XX KW Human; heparanase; heparanase-dependent cancer; cancer;  
XX KW autoimmune reaction; inflammation; chromosome 4; enzyme.  
XX OS Homo sapiens.  
XX PN US2003236215-A1.



XX PD 25-DEC-2003.  
 XX PF 09-JUN-2003; 2003US-00456573.  
 XX 31-AUG-1998; 98WO-US017954.  
 XX 01-MAR-1999; 99US-00258892.  
 XX 08-NOV-1999; 99US-00435739.  
 XX (INSI-) INSIGHT STRATEGY & MARKETING LTD.  
 XX (HADA-) HADASIT MEDICAL RES SERVICES & DEV.  
 XX Pecker I, Vlodavsky I, Feinstein E;  
 XX WPI; 2004-070610/07.  
 XX New antisense oligonucleotide hybridizable with a polynucleotide encoding  
 PT a polypeptide with heparanase activity, useful for treating diseases such  
 PT as cancer and autoimmune disorders.  
 XX Claim 3; SEQ ID NO 14; 108pp; English.

XX The invention relates to an antisense oligonucleotide (ASO) comprising a  
 CC polynucleotide or a polynucleotide analogue of at least 10 bases being  
 CC hybridisable in vivo, under physiological conditions, with a portion of  
 CC a polynucleotide strand encoding a polypeptide having heparanase  
 CC catalytic activity. Also included are a method of in vivo downregulating  
 CC heparanase activity (comprising administering the ASO in vivo), a method  
 CC of treating a subject suffering from a pathological condition  
 CC (characterised by heparanase activity, comprising administering ASO to  
 CC the subject), a pharmaceutical composition comprising the ASO and a  
 CC carrier, an antisense nucleic acid construct (comprising a promoter  
 CC sequence and a polynucleotide sequence directing the synthesis of an  
 CC antisense RNA sequence of at least 10 bases being hybridisable in vivo,  
 CC under physiological conditions, with a polynucleotide strand encoding a  
 CC polypeptide having heparanase catalytic activity), a method of in vivo  
 CC downregulating heparanase activity (comprising administering in vivo the  
 CC antisense nucleic acid construct), a pharmaceutical composition  
 CC comprising the antisense nucleic acid construct and a carrier, and an  
 CC antisense oligonucleotide comprising a polynucleotide or a polynucleotide  
 CC analogue of at least 10 bases being hybridisable in vivo, under  
 CC physiological conditions, with a portion of a polynucleotide strand being  
 CC characterised by forming at least a portion of an untranslated region  
 CC (UTR) for a polynucleotide strand encoding a polypeptide having  
 CC heparanase catalytic activity. The methods and compositions of the  
 CC present invention are useful for the prevention and/or treatment of  
 CC diseases or conditions associated with aberrant heparanase activity, such  
 CC as heparanase-dependent cancer, cancer, autoimmune reaction and  
 CC inflammation. The gene for human heparanase is located on chromosome 4.  
 CC The present sequence is a human heparanase protein.

XX SQ Sequence 592 AA;

Query Match 100.0%; Score 2842; DB 8; Length 592;  
 Best Local Similarity 100.0%; Pred. No. 3.3e-273;  
 Matches 543; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLLRSKALPPPLMLLLGLPLSPGALPRPAQADVDLDFPTQPLHLVSPFLSVT 60  
 Db 50 MLLRSKALPPPLMLLLGLPLSPGALPRPAQADVDLDFPTQPLHLVSPFLSVT 109  
 Qy 61 IDANLATDPRFLILGSPKLTLAGLSPAYLRFGGTKTDFLFDPKKSTFEERSYQWS 120  
 Db 110 IDANLATDPRFLILGSPKLTLAGLSPAYLRFGGTKTDFLFDPKKSTFEERSYQWS 169  
 Qy 121 QVNQDICKYGSIPDPVEEKLRLWPYQEQLLREHYQKFKNSTYSSVDVLYTFANCS 180  
 Db 170 QVNQDICKYGSIPDPVEEKLRLWPYQEQLLREHYQKFKNSTYSSVDVLYTFANCS 229  
 Qy 181 GLDLIFGLNALLRTADLQWNSNAQLLDYCSSKGYNISWELGNPNFSFLKKADIFNGS 240  
 Db 230 GLDLIFGLNALLRTADLQWNSNAQLLDYCSSKGYNISWELGNPNFSFLKKADIFNGS 289

Qy 241 QLGEDYIQLHKLRLKSTFKNAKLYGPDVGQPRRKTAOMLKSFLKAGGEVIDSVTHHHYL 300  
 Db 290 QLGEDYIQLHKLRLKSTFKNAKLYGPDVGQPRRKTAOMLKSFLKAGGEVIDSVTHHHYL 349  
 Qy 301 NGRTATREDFLNPDVLDIFISSVQKVQVVESTRPGKKVWLGETSSAYGCGAPLLSDTEA 360  
 Db 350 NGRTATREDFLNPDVLDIFISSVQKVQVVESTRPGKKVWLGETSSAYGCGAPLLSDTEA 409  
 Qy 361 AGFMWLDKLGLSARMGIEVVMRQVFFGAGNYHLVDENFDPLPDYWLSSLFKKLVTGTVLM 420  
 Db 410 AGFMWLDKLGLSARMGIEVVMRQVFFGAGNYHLVDENFDPLPDYWLSSLFKKLVTGTVLM 469  
 Qy 421 ASVQSGSKRRKRLRVYLHCTNTDNPYKEGDLTLVAINLHNVTYKYLRLPYPSNKKQVDKYL 480  
 Db 470 ASVQSGSKRRKRLRVYLHCTNTDNPYKEGDLTLVAINLHNVTYKYLRLPYPSNKKQVDKYL 529  
 Qy 481 RPLGPHGLLSKSVQLNGLTLKMWDDOTLPLMEKPLRPGSSGLGPAFYSYFFVIRNAKVA 540  
 Db 530 RPLGPHGLLSKSVQLNGLTLKMWDDOTLPLMEKPLRPGSSGLGPAFYSYFFVIRNAKVA 589  
 Qy 541 ACI 543  
 Db 590 ACI 592  
 RESULT 15  
 ADM48720  
 ID ADM48720 standard; protein; 592 AA.  
 XX ADM48720;  
 AC ADM48720;  
 DT 03-JUN-2004 (first entry)  
 XX Human SK-hepl hpa protein.  
 DE Human SK-hepl hpa protein.  
 XX Transgenic animal; heparanase; cancer; viral infection; restenosis;  
 KW neurodegenerative disease; atherosclerosis; pulmonary disorder; hpa;  
 KW human.  
 KW Homo sapiens.  
 OS Homo sapiens.  
 XX US2003217375-A1.  
 PN 20-NOV-2003.  
 XX 24-FEB-2003; 2003US-00371218.  
 PF 31-AUG-1998; 98WO-US017954.  
 PR 01-MAR-1999; 99US-00258892.  
 PR 06-FEB-2001; 2001US-00776874.  
 PR 19-NOV-2001; 2001US-00988113.  
 XX (ZCHA/) ZCHARIA E.  
 PA (VLOD/) VLODAVSKY I.  
 PA (METZ/) METZGER S.  
 PA (PECK/) PECKER I.  
 PA (ILAN/) ILAN N.  
 PA (CHAJ/) CHAJEK-SHAUL T.  
 PA (GOLD/) GOLDSHMIDT O.  
 XX Zcharia E, Vlodavsky I, Metzger S, Pecker I, Ilan N;  
 PI Chajek-Shaul T, Goldshmidt O;  
 XX WPI; 2004-021918/02.  
 DR N-PSDB; ADM48719, ADM48721.  
 XX New transgenic non-human animal expressing heparinase, useful as models  
 PT for human disease, such as cancer, viral infection, neurodegenerative  
 PT diseases, restenosis, atherosclerosis and pulmonary disorders.  
 XX Example 6; SEQ ID NO 14; 106pp; English.  
 XX The present invention relates to a transgenic non-human animal whose



GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.  
OM protein - protein search, using sw model  
Run on: February 27, 2006, 17:31:41 ; Search time 234 Seconds  
(without alignments)  
1637.187 Million cell updates/sec  
Title: US-10-676-079-2  
Perfect score: 2842  
Sequence: 1 MLRSKPALPPPLMLLLGP.....LPAFSYFFVIRNAKVAACI 543  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5  
Searched: 2166443 seqs, 705528306 residues  
Total number of hits satisfying chosen parameters: 2166443  
Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries  
Database : Uniprot\_05.80.\*  
1: uniprot\_sprot.\*  
2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2838	99.9	543	Q9Y251_HUMAN	Q9Y251 homo sapien
2	2831	99.6	543	Q53GE5_HUMAN	Q53GE5 homo sapien
3	2817	99.1	545	Q9UL39_HUMAN	Q9UL39 homo sapien
4	2282	80.3	545	Q9MY70_BOVIN	Q9MY70 bos taurus
5	2150	75.7	535	Q8K3K3_MOUSE	Q8K3K3 mus musculus
6	2140	75.3	535	Q6YGG1_MOUSE	Q6YGG1 mus musculus
7	2135	75.1	536	Q71RP1_RAT	Q71RP1 rattus norv
8	2123	74.7	536	Q9QZP8_RAT	Q9QZP8 rattus norv
9	1645.5	57.9	523	Q90YK5_CHICK	Q90YK5 gallus gall
10	1317	46.3	533	Q4SYF6_TETNG	Q4SYF6 tetraodon n
11	1154.5	40.6	592	Q9HB37_HUMAN	Q9HB37 homo sapien
12	1151.5	40.5	592	Q5VUH6_HUMAN	Q5VUH6 homo sapien
13	1146.5	40.3	592	Q8WMQ2_HUMAN	Q8WMQ2 homo sapien
14	1040.5	36.6	597	Q4TB80_TETNG	Q4TB80 tetraodon n
15	1021.5	35.9	548	Q5VUH4_HUMAN	Q5VUH4 homo sapien
16	1015.5	35.7	548	Q8WQ1_HUMAN	Q8WQ1 homo sapien
17	936.5	33.0	534	Q9HB38_HUMAN	Q9HB38 homo sapien
18	933.5	32.8	534	Q5VUH5_HUMAN	Q5VUH5 homo sapien
19	897.5	31.6	480	Q9HB39_HUMAN	Q9HB39 homo sapien
20	739.5	26.0	255	Q4TGC8_TETNG	Q4TGC8 tetraodon n
21	696	24.5	515	Q8T108_BOMMO	Q8T108 bombyx mori
22	416	14.6	521	Q9SDAL_ARATH	Q9SDAL arabidopsis
23	416	14.6	543	Q9FF10_ARATH	Q9FF10 arabidopsis
24	404	14.2	559	Q89F99_BRAJA	Q89F99 bradyrhizob
25	388	13.7	526	Q5SNA6_ORYSA	Q5SNA6 oryza sativ
26	381	13.4	527	Q9LRC8_SCUBA	Q9LRC8 scutellaria
27	379	13.3	541	Q69116_ORYSA	Q69116 oryza sativ
28	364	12.8	537	Q70YJ3_HORVU	Q70YJ3 hordeum vul
29	363	12.8	536	Q9FZP1_ARATH	Q9FZP1 arabidopsis
30	352.5	12.4	516	Q9FLK8_ARATH	Q9FLK8 arabidopsis
31	352.5	12.4	539	Q8L608_ARATH	Q8L608 arabidopsis

RESULT 1  
Q9Y251\_HUMAN  
ID Q9Y251\_HUMAN PRELIMINARY; PRT; 543 AA.  
AC Q9Y251\_HUMAN  
DT 01-NOV-1999 (Tremblrel. 12, Created)  
DT 01-NOV-1999 (Tremblrel. 12, Last sequence update)  
DT 10-MAY-2005 (Tremblrel. 30, Last annotation update)  
DE Heparanase.  
GN Name=HPA; Synonyms=HPSE;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Placenta;  
RX MEDLINE=99321249; PubMed=10395326; DOI=10.1038/10525;  
RA Hulett M.D., Freeman C., Hamdorf B.J., Baker R.T., Harris M.J., Parish C.R.;  
RT "Cloning of mammalian heparanase, an important enzyme in tumor invasion and metastasis.";  
RL Nat. Med. 5:803-809(1999).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Placenta;  
RX MEDLINE=99335379; PubMed=10405343; DOI=10.1006/bbrc.1999.0962;  
RA Kussie P.H., Hulmes J.D., Ludwig D.L., Patel S., Navarro E.C., Seddon A.P., Giorgio N.A., Bohlen P.;  
RA Seddon A.P., Giorgio N.A., Bohlen P.;  
RT "Cloning and functional expression of a human heparanase gene.";  
RL Biochem. Biophys. Res. Commun. 261:183-187(1999).  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Placenta;  
RX MEDLINE=99377052; PubMed=10446189; DOI=10.1074/jbc.274.34.24153;  
RA Toyoshima M., Nakajima M.;  
RT "Human heparanase. Purification, characterization, cloning, and expression.";  
RL J. Biol. Chem. 274:24153-24160(1999).  
RN [5]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Pancreas;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

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RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McWen P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA *lakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimmutz J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Marra M.A.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [6]
RN RESULT 2
RP O53GES HUMAN PRELIMINARY; PRT; 543 AA.
AC O53GES;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DB Heparanase variant (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE
RC TISSUE=Human small intestine;
RA Maruyama K., Sugano S.;
RT "Oligo-capping: a simple method to replace the cap structure of
RT eucaryotic mRNAs with oligoribonucleotides.";
RL Gene 138:171-174 (1994).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Human small intestine;
RA Suzuki Y., Yoshitomo K., Maruyama K., Sugano A., Sugano S.;
RT "Construction and characterization of a full length-enriched and a 5'-
RT end-enriched cDNA library.";
RL Gene 200:149-156 (1997).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Human small intestine;
RA Suzuki Y., Sugano S., Totoki Y., Toyoda A., Takeda T., Sakaki Y.,
RA Tanaka A., Yokoyama S.;
RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK222986; BAD96706.1; -; mRNA.
FT NON_TER
SQ SEQUENCE 543 AA; 61118 MW; AC392EC267FC4AB2 CRC64;
Query Match 99.6%; Score 2831; DB 2; Length 543;
Best Local Similarity 99.6%; Pred. No. 4.8e-203;
Matches 541; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 MLLRSKPALPPMLLLGLPLSPGALPRPAQAQDVVDLDFFTQEPHLHVSFSLSVT 60
DB 1 MLLRSKPALPPMLLLGLPLSPGALPRPAQAQDVVDLDFFTQEPHLHVSFSLSVT 60
QY 61 IDANLATDPRFLIILGSPKRLTARGLSPAYLRFGGTKTDFLIIDPKKESTFEERSYQWS 120
DB 61 IDANLATDPRFLIILGSPKRLTARGLSPAYLRFGGTKTDFLIIDPKKESTFEERSYQWS 120
QY 121 QVNQDICKYGSIPDPVEKRLRWPYQQLLREHYQKFNKNSTYSRSSVDVLYTFNACS 180
DB 121 QVNQDICKYGSIPDPVEKRLRWPYQQLLREHYQKFNKNSTYSRSSVDVLYTFNACS 180
QY 181 GLDLIFGLNALLRTADLQWNSSNAQLLLDYCSSKGYNISWELGNPNFLKADIFINGS 240
DB 181 GLDLIFGLNALLRTADLQWNSSNAQLLLDYCSSKGYNISWELGNPNFLKADIFINGS 240
QY 241 QLGEDYIQLHKLKRSTFKNAKLYGPDVGQPRRTAKMLKSLFKAGGEVIDSVTWHYYL 300
DB 241 QLGEDYIQLHKLKRSTFKNAKLYGPDVGQPRRTAKMLKSLFKAGGEVIDSVTWHYYL 300
QY 421 ASVQGSKRRLRVYLHCTNTDNPRYKEGDLTLVAINLHNVTKYLRLPYPFSSNKQVDKYLL 480
DB 421 ASVQGSKRRLRVYLHCTNTDNPRYKEGDLTLVAINLHNVTKYLRLPYPFSSNKQVDKYLL 480
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McWen P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA *lakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimmutz J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Marra M.A.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [6]
RN RESULT 2
RP O53GES HUMAN PRELIMINARY; PRT; 543 AA.
AC O53GES;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DB Heparanase variant (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE
RC TISSUE=Human small intestine;
RA Maruyama K., Sugano S.;
RT "Oligo-capping: a simple method to replace the cap structure of
RT eucaryotic mRNAs with oligoribonucleotides.";
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RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Human small intestine;
RA Suzuki Y., Yoshitomo K., Maruyama K., Sugano A., Sugano S.;
RT "Construction and characterization of a full length-enriched and a 5'-
RT end-enriched cDNA library.";
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RN [3]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Human small intestine;
RA Suzuki Y., Sugano S., Totoki Y., Toyoda A., Takeda T., Sakaki Y.,
RA Tanaka A., Yokoyama S.;
RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK222986; BAD96706.1; -; mRNA.
FT NON_TER
SQ SEQUENCE 543 AA; 61177 MW; AD262EC267334AB2 CRC64;
Query Match 99.9%; Score 2838; DB 2; Length 543;
Best Local Similarity 99.8%; Pred. No. 1.4e-203;
Matches 542; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLLRSKPALPPMLLLGLPLSPGALPRPAQAQDVVDLDFFTQEPHLHVSFSLSVT 60
DB 1 MLLRSKPALPPMLLLGLPLSPGALPRPAQAQDVVDLDFFTQEPHLHVSFSLSVT 60
QY 61 IDANLATDPRFLIILGSPKRLTARGLSPAYLRFGGTKTDFLIIDPKKESTFEERSYQWS 120
DB 61 IDANLATDPRFLIILGSPKRLTARGLSPAYLRFGGTKTDFLIIDPKKESTFEERSYQWS 120
QY 121 QVNQDICKYGSIPDPVEKRLRWPYQQLLREHYQKFNKNSTYSRSSVDVLYTFNACS 180
DB 121 QVNQDICKYGSIPDPVEKRLRWPYQQLLREHYQKFNKNSTYSRSSVDVLYTFNACS 180
QY 181 GLDLIFGLNALLRTADLQWNSSNAQLLLDYCSSKGYNISWELGNPNFLKADIFINGS 240
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DB 241 QLGEDYIQLHKLKRSTFKNAKLYGPDVGQPRRTAKMLKSLFKAGGEVIDSVTWHYYL 300
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DB 301 NGRATREDFLNPVDLDFIISVQKVFQVVESTRPCKKVMIGETSSAYGGGAPLLSDTFA 360
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DB 361 AGFMWLDKGLSARGMGIWVRQVFFGAGNHLVDENFDPLPDYWLSSLFKLVGTVM 420
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DB 421 ASVQGSKRRLRVYLHCTNTDNPRYKEGDLTLVAINLHNVTKYLRLPYPFSSNKQVDKYLL 480
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Db |||||  
Qy 361 AGFWLMDKLGLSARMGIEVVMRQVFFGAGNHYLVDENFDPLPDYWLKLLFKKLVTGTVLM 420  
Db |||||  
Qy 361 AGFWLMDKLGLSARMGIEVVMRQVFFGAGNHYLVDENFDPLPDYWLKLLFKKLVTGTVLM 420  
Db |||||  
Qy 421 ASVQSGSKRKLRVYLHCTNTNDNPRYKEGDLTLAYAINLHNVTKYLRLLPYFNSNKQVDKYL 480  
Db |||||  
Qy 421 ASVQSGSKRKLRVYLHCTNTNDNPRYKEGDLTLAYAINLHNVTKYLRLLPYFNSNKQVDKYL 480  
Db |||||  
Qy 481 RPLGPHGLSKSVQNLGLTLKXVDDQTLPLPMEKPLRPGSSGLGPAFYSFFVIRNAKVA 540  
Db |||||  
Qy 481 RPLGPHGLSKSVQNLGLTLKXVDDQTLPLPMEKPLRPGSSGLGPAFYSFFVIRNAKVA 540  
Db |||||  
Qy 541 ACI 543  
Db |||||  
Qy 541 ACI 543  
Db |||||

RESULT 3  
Q9UL39\_HUMAN  
ID Q9UL39\_HUMAN PRELIMINARY; PRT; 545 AA.  
AC Q9UL39;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE Heparanase.  
GN Name=HPSE;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Placenta;  
RX MEDLINE=20229546; PubMed=10764835; DOI=10.1093/glycob/10.5.467;  
RA Dempsey L.A., Plummer T.B., Coombes S.L., Platt J.L.;  
RT "Heparanase expression in invasive trophoblasts and acute vascular  
RT damage.";  
RL Glycobiology 10:467-475 (2000).  
DR EMBL; AF084467; AAD54516.1; -; mRNA.  
DR Ensembl; ENSG00000173083; Homo sapiens.  
DR HGNC; HGNC:5164; HPSE.  
DR InterPro; IPR005199; Glyco\_hydro\_79N.  
DR Pfam; PF03662; Glyco\_hydro\_79n; I.  
SQ SEQUENCE 545 AA; 61417 MW; 67B80ACD73C5A9A1 CRC64;

Query Match 99.1%; Score 2817; DB 2; Length 545;  
Best Local Similarity 99.4%; Pred. No. 5.4e-202; Mismatches 0; Indels 2; Gaps 2;  
Matches 542; Conservative 1; Mismatches 0; Indels 2; Gaps 2;  
Qy 1 MLRSKALPPP-LMLLLGLPLGSPALPRPQA-QDVVDLDFFTQEPHLHVSFSL 58  
Db |||||  
Qy 1 MLRSKALPPP-LMLLLGLPLGSPALPRPQA-QDVVDLDFFTQEPHLHVSFSL 60  
Db |||||  
Qy 59 VTIDANLATDPRFLILGSPKLTARGLSPAYLRFGGTKTDFLIFDPKKESTFEERSY 118  
Db |||||  
Qy 61 VTIDANLATDPRFLILGSPKLTARGLSPAYLRFGGTKTDFLIFDPKKESTFEERSY 120  
Db |||||  
Qy 119 QSOVNDICKGSIPDPVEEKLREWPYQEQLLREHYQKKFNSTYSRSSVDVLYTFAN 178  
Db |||||  
Qy 121 QSOVNDICKGSIPDPVEEKLREWPYQEQLLREHYQKKFNSTYSRSSVDVLYTFAN 180  
Db |||||  
Qy 179 CSGLDLIFGLNALTADLQWSSNAQLLDYCSSKGYNISWELGNEPNSFLKKADIFIN 238  
Db |||||  
Qy 181 CSGLDLIFGLNALTADLQWSSNAQLLDYCSSKGYNISWELGNEPNSFLKKADIFIN 240  
Db |||||  
Qy 239 GSQLGEDYIQLHKLRLKSTFKNAKLYGPDVGQPRRTAKMLKSPFKAGGEVIDSVTWHY 298  
Db |||||  
Qy 241 GSQLGEDYIQLHKLRLKSTFKNAKLYGPDVGQPRRTAKMLKSPFKAGGEVIDSVTWHY 300  
Db |||||

Qy 299 YLNGRTATREDFLNPDVLDIFISSVQKVFQVVESTPRGKKVWLGETSSAYGGAPLLSDT 358  
Db |||||  
Qy 301 YLNGRTATREDFLNPDVLDIFISSVQKVFQVVESTPRGKKVWLGETSSAYGGAPLLSDT 360  
Db |||||  
Qy 359 FAAGFWLMDKLGLSARMGIEVVMRQVFFGAGNHYLVDENFDPLPDYWLKLLFKKLVTGTV 418  
Db |||||  
Qy 361 FAAGFWLMDKLGLSARMGIEVVMRQVFFGAGNHYLVDENFDPLPDYWLKLLFKKLVTGTV 420  
Db |||||  
Qy 419 LMASVQSGSKRKLRVYLHCTNTNDNPRYKEGDLTLAYAINLHNVTKYLRLLPYFNSNKQVDKY 478  
Db |||||  
Qy 421 LMASVQSGSKRKLRVYLHCTNTNDNPRYKEGDLTLAYAINLHNVTKYLRLLPYFNSNKQVDKY 480  
Db |||||  
Qy 479 LRLPGLPHGLSKSVQNLGLTLKXVDDQTLPLPMEKPLRPGSSGLGPAFYSFFVIRNAK 538  
Db |||||  
Qy 481 LRLPGLPHGLSKSVQNLGLTLKXVDDQTLPLPMEKPLRPGSSGLGPAFYSFFVIRNAK 540  
Db |||||  
Qy 539 VAACI 543  
Db |||||  
Qy 541 VAACI 545  
Db |||||

RESULT 4  
Q9MY10\_BOVIN  
ID Q9MY10\_BOVIN PRELIMINARY; PRT; 545 AA.  
AC Q9MY10;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE Heparanase.  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;  
OC Pecora; Bovidae; Bovinae; Bos.  
OX NCBI\_TaxID=9913;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Placenta;  
RX MEDLINE=21176669; PubMed=11277877;  
RA Kizaki K., Nakano H., Nakano H., Takahashi T., Imai K., Hashizume K.;  
RT "Expression of heparanase mRNA in bovine placenta during gestation.";  
RL Reproduction 121:573-580 (2001).  
DR EMBL; AF281160; AAF87301.2; -; mRNA.  
DR InterPro; IPR005199; Glyco\_hydro\_79N.  
DR Pfam; PF03662; Glyco\_hydro\_79n; I.  
SQ SEQUENCE 545 AA; 61076 MW; FAC4BDPFD855B933 CRC64;

Query Match 80.3%; Score 2282; DB 2; Length 545;  
Best Local Similarity 79.8%; Pred. No. 6.1e-162;  
Matches 435; Conservative 35; Mismatches 73; Indels 2; Gaps 1;  
Qy 1 MLRSKALPPP-LMLLLGLPLGSPALPRPQA-QDVVDLDFFTQEPHLHVSFSL 58  
Db |||||  
Qy 1 MLRSKALPPP-LMLLLGLPLGSPALPRPQA-QDVVDLDFFTQEPHLHVSFSL 60  
Db |||||  
Qy 59 VTIDANLATDPRFLILGSPKLTARGLSPAYLRFGGTKTDFLIFDPKKESTFEERSY 118  
Db |||||  
Qy 61 VTIDANLATDPRFLILGSPKLTARGLAPAYLRFGGNKGDFLIIDPKKEPAFEERSY 120  
Db |||||  
Qy 119 QSOVNDICKGSIPDPVEEKLREWPYQEQLLREHYQKKFNSTYSRSSVDVLYTFAN 178  
Db |||||  
Qy 121 LSQSNODICKSGSIPSDVEEKLREWPYQEQVLLREYQKKFTNSTYSRSSVDVLYTFAS 180  
Db |||||  
Qy 179 CSGLDLIFGLNALTADLQWSSNAQLLDYCSSKGYNISWELGNEPNSFLKKADIFIN 238  
Db |||||  
Qy 181 CSGLDLIFGLNALTADLQWSSNAQLLDYCSSKGYNISWELGNEPNSFQKAGIFIN 240  
Db |||||  
Qy 239 GSQLGEDYIQLHKLRLKSTFKNAKLYGPDVGQPRRTAKMLKSPFKAGGEVIDSVTWHY 298  
Db |||||  
Qy 241 GSQLGEDYIQLHKLRLKSTFKNAKLYGPDVGQPRRTAKMLKSPFKAGGEVIDSVTWHY 300  
Db |||||  
Qy 299 YLNGRTATREDFLNPDVLDIFISSVQKVFQVVESTPRGKKVWLGETSSAYGGAPLLSDT 358  
Db |||||

Db 301 YVNGRIATKDFLNPDLDTFISSVQKTRIVEKIRPLKVKWLGETSAPGGAPFLSNT 360  
Qy 359 FAAGFMWLDKLGISARMGIEVWNRQVFGAGNYHLVDENFPDPLDDYWLSSLFLPKLVGTVK 418  
Db 361 FAAGFMWLDKLGISARMGIEVWNRQVLFAGAGNYHLVDGNFPDPLDDYWLSSLFLPKLVGNKV 420  
Qy 419 LMASVOGSKRKLRYVLLHCTTNDPNRYKEGDLTLVAINLHNVTKYLRPLPYFPFSKNQVDKY 478  
Db 421 LMASVKGDPDRSKFRVYLLHCTTNDPNRYKEGDLTLVAINLHNVTKYLRPLPYFPFSKNQVDKY 480  
Qy 479 LLRLPGLHGLSKSVQLNGLTLMKWDQTLPLMEKPLRPGSSGLGPAFYSFFVIRNAK 538  
Db 481 LIKPSGTDLGLSKSVQLNGLTLMKWDQTLPLMEKPLRPGSSGLGPAFYSFFVIRNAK 540  
Qy 539 VAACI 543  
Db 541 VAACI 545  
RESULT 5  
Q8K3K3\_MOUSE  
ID Q8K3K3\_MOUSE PRELIMINARY; PRT; 535 AA.  
AC Q8K3K3;  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)  
DE Heparanase (Mus musculus 0 day neonate thymus cDNA, RIKEN full-length  
DE enriched library, clone:A43010M04 product:heparanase, full insert  
DE sequence).  
GN Name:Hps; Synonyms:Hpa, Hspe;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muridae; Murinae; Mus.  
OC NCBI TaxID=10090;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=FBV;  
RA Miao H.-Q., Navarro E., Patel S., Sargent D., Koo H., Wan H.,  
RA Plata A.-Q., Zhou Q., Ludwig D., Bohlen P., Kussie P.;  
RT "Cloning, expression, and purification of mouse heparanase";  
RL Protein Expr. Purif. 0:0-0(2002).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J; TISSUE=Thymus;  
RX MEDLINE=21085660; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;  
RA Carninci P., Hayashizaki Y.;  
RT "High-efficiency full-length cDNA cloning";  
RL Meth. Enzymol. 303:19-44(1999).  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J; TISSUE=Thymus;  
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;  
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,  
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,  
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,  
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,  
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,  
RA Schriml L.M., Staubli F., Suzuki R., Tonita M., Wagner L., Washio T.,  
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,  
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,  
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,  
RA Gustincich S., Hill D., Hofmann C., Hume D.A., Kamiya M., Lee N.H.,  
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,  
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,  
RA Suzuki H., Toyooka K., Wang K.H., Weltz C., Whittaker C., Wilming L.,  
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,  
RA Hayashizaki Y.;  
RT "Functional annotation of a full-length mouse cDNA collection";  
RL Nature 409:685-690(2001).

RN NUCLEOTIDE SEQUENCE.  
RP STRAIN=C57BL/6J; TISSUE=Thymus;  
RX MEDLINE=22354683; PubMed=12468851; DOI=10.1038/nature01266;  
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,  
RA Nikaide I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,  
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,  
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,  
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,  
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,  
RA Dalla E., Dragani T.A., Fletcher C., Forrest A., Frazer K.S.,  
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,  
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,  
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,  
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,  
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,  
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,  
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramchandran S.,  
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,  
RA Sadelin A., Schneider C., Semple C.A., Setou M., Shimada K.,  
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tonita M.,  
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,  
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang L., Yang L.,  
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,  
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,  
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,  
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,  
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,  
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,  
RA Birney E., Hayashizaki Y.;  
RT "Analysis of the mouse transcriptome based on functional annotation of  
RT 60,770 full-length cDNAs";  
RL Nature 420:563-573(2002).  
RN [5]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J; TISSUE=Thymus;  
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;  
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,  
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;  
RT "Normalization and subtraction of cap-trapper-selected cDNAs to  
RT prepare full-length cDNA libraries for rapid discovery of new genes";  
RL Genome Res. 10:1617-1630(2000).  
RN [6]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J; TISSUE=Thymus;  
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;  
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,  
RA Konno H., Akiyama J., Nishi K., Kitsuunai T., Tashiro H., Itoh M.,  
RA Suni N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,  
RA Yamamoto R., Matsunoto H., Sakaguchi S., Ikegami T., Kaehiwagi K.,  
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,  
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,  
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;  
RT "RIKEN integrated sequence analysis (RISA) system-384-format  
RT sequencing pipeline with 384 multicapillary sequencer";  
RL Genome Res. 10:1757-1771(2000).  
RN [7]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J; TISSUE=Thymus;  
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;  
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,  
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,  
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,  
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,  
RA Kato H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,  
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,  
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,  
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,  
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,  
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,  
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;  
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
RN [8]  
RP NUCLEOTIDE SEQUENCE.

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RESULT 6
Q6YGZ1_MOUSE
ID Q6YGZ1_MOUSE PRELIMINARY;  PET;  535 AA.
AC Q6YGZ1;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hepaxanase.
GN Name:Hpsse
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
[1]
RN NUCLEOTIDE SEQUENCE.
RP
RP MEDLINE=22841152; PubMed=12837765; DOI=10.1074/jbc.M300925200;
RX
RX Gong F., Galvis M.L.E., Vlodavsky I., Horner A., Lindahl U.,

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RESULT	7
Q71RP1_RAT	
ID	Q71RP1_RAT PRELIMINARY; PRT; S36 AA.
AC	Q71RP1;
DT	05-JUL-2004 (T=EMBLrel. 27, Created)
DT	05-JUL-2004 (T=EMBLrel. 27, Last sequence update)
DT	05-JUL-2004 (T=EMBLrel. 27, Last annotation update)
DE	Heparanase.
GN	Name:Hpsae; Synonym:sHepe;
OS	Rattus norvegicus (Rat)
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC	Muridae; Murinae; Rattus.
OX	NCBI_TaxID=10116;
[1]	-
RN	NUCLEOTIDE SEQUENCE.
RA	Hulett M.D., Wang J., Hornby J.R., Freeman C., Pagler E., McHenry J.,
RA	Parish C.R.;





Query Match 57.9%; Score 1645.5; DB 2; Length 523;  
 Best Local Similarity 60.2%; Pred. No. 2.5e-114;  
 Matches 320; Conservative 87; Mismatches 114; Indels 11; Gaps 3;

QY 13 LMLLLGLPLGSLPRPAQADVDLDFEOTPEHLVSPSLVTIDANLATDREL 72  
 DB 2 LVLLLVLLAVPP-----RTAEQLQGLREPIGAVSPALSTLDASLARDPRFV 52  
 QY 73 ILLGSPKLRTLARGSLPAYLRFQGTCTDFLIFDPKKESTPEERSYQSQVNDICIKYGS 132  
 DB 53 ALLRHPLKHLTLASGLSPGLRFQGTCTDFLIFDNKDWEEKVSEFQA-KOVCEAWPS 111  
 QY 133 PPVVEEKLRLWEPYQEBQLELLREHYQKFKNSTYSRSSVDVLYTFANCGLDLIFGLNALL 192  
 DB 112 FAVVPKLLLTQWPLQEBKLLAEHSWKXKNTTITRSTLDLHTFPASSGFRFLVGLNALL 171  
 QY 193 RTADLWNSSNAQLLDYCSKGYNISWELGNEPNSFKKADIPIFNGSOLGEDYIQLHLK 252  
 DB 172 RRAGLWDSSNAQLLGYCAQRSYNIWELGNEPNSFRKSGICIDFQGLORDFVHLRQL 231  
 QY 253 L-RKSTFKNALYGPDYQGPRTAKMLKSLFKAGGEVIDSVTWHYHLYNGRTATREDFL 311  
 DB 232 LSQHPYRHAELYGLDVQGPRTQHLLRSFPMKSGKAIDSVTWHYHLYNGRSATREDFL 291  
 QY 312 NPVDLDFISVQVQFQVVESTRPGKVKWLGESTSSAYGGGAPLSDTFAAGFMWLDKGL 371  
 DB 292 SPEVLDSPATAIHDPVLGVEATPGKVKWLGESTSGAYGGGAPLSDTFAAGFMWLDKGL 351  
 QY 372 SARAGIEVWROVFEGAGNHLVDENFDPLDYLWLSLFLFKLVCTKVLMAVQSGSKRL 431  
 DB 352 AARGIDVWROVQSGAGSVHLVDAGPKPLDYLWLSLFLFKLVCTKVLMAVQSGSKRL 411  
 QY 432 RVLHCTNTDPRYKEGDLTLVAINLHNVTKLRLPYFPFNGKQVDKYLRLPLGPHGLSK 491  
 DB 412 RVLHCTNPRPKYREGDVTLPALNSVNTQSLQPKQLMSKSDVDYLLPHGKDSILSR 471  
 QY 492 SVQLNGLTKMVDQDTLPPLMEKPLRPGSSGLPAPFSYFVIRNAKVAACI 543  
 DB 472 EVQLNGRLQWDDDETLPALHEMALAPGSTLGLPAPFSYFVIRNAKVAACI 523

## RESULT 10

Q4SYF6\_TETNG  
 ID Q4SYF6\_TETNG PRELIMINARY; PRT; 533 AA.  
 AC Q4SYF6;  
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)  
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)  
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)  
 DE Chromosome undetermined SCAF12073, whole genome shotgun sequence.  
 DE (Frames)  
 GN ORFNames=GSTENG0010356001;  
 OS Tetraodon nigroviridis (Green puffer).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
 OC Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;  
 OC Tetraodontidae; Tetraodontidae; Tetraodon.  
 OX NCBI\_TaxID=99883;  
 RN [1]

## NUCLEOTIDE SEQUENCE.

RP Jallou O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,  
 RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,  
 RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segures B.,  
 RA Dagiva C., Salanoubat M., Levy M., Boudet N., Castellano S.,  
 RA Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,  
 RA Blemont C., Skalli Z., Cottolico L., Poullain J., De Berardinis V.,  
 RA Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,  
 RA Kellis M., Volff J.N., Guigo R., Zody M.C., Mesirov J.,  
 RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,  
 RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,  
 RA Winkler P., Lander E.S., Weissenbach J., Roest Crolius H.,  
 RA "Genome duplication in the teleost fish Tetraodon nigroviridis reveals  
 RT the early vertebrate proto-karyotype.";

RL Nature 431:946-957 (2004).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RG Genoscope; Whitehead Institute Centre for Genome Research;  
 RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.  
 CC -1- CAUTION: The sequence shown here is derived from an  
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
 CC preliminary data.  
 CC EMBL; CAAE01012073; CAF94326.1; -; Genomic\_DNA.  
 DR NON\_TER 1 1  
 FT NON\_TER 533 533  
 SQ SEQUENCE 533 AA; 60100 MW; 9800A7C8780100FF CRC64;

Query Match 46.3%; Score 1317; DB 2; Length 533;  
 Best Local Similarity 50.0%; Pred. No. 1e-89;  
 Matches 268; Conservative 83; Mismatches 141; Indels 44; Gaps 8;

QY 49 LHLVSPSLVTIDANLATDPRLLILGSPKLTLAGLSPAYLRFQGTCTDFLIPPK 108  
 DB 1 LRRVDPRLVSTIDASLAADERFMYLLSSPKVTLAKALTPAFLRFGTQDFMVFAPHK 60  
 QY 109 E---STPEERSYQSQVNDICIKYGSIPDPVEEKLRLWEPYQEBQLELLREHYQKFKNSTY 165  
 DB 61 NQPASGFSARELTFSSNGQHSCEWAPPWLERRRLRTEWKKQWMLRNEBQRYRVPK 120  
 QY 166 SRSSVDVLYTFANCGLDLIFGLNALLRTADLQWSSNAQLLDYCSKGYNISWELGNE 225  
 DB 121 TETTVQQLHAFANCGLDLVFLNALLRTADLQWSSNAQLLDYCSKGYNISWELGNE 180  
 QY 226 PNLFLKADIPIFNGSOLGEDYIQLHLKRLKSTF-KNAKLYGDPVQGPRTAKMLSKFLK 284  
 DB 181 PNSYEKAGLRLDGRQLGEDFTVLRKTLRESRFYRDAGLFGDPVQGPDRHIDILSGFLQ 240  
 QY 285 AGGEVIDSVTWHYHLYNGRTATREDFLNPDVLDIFISSVQKVFQVVESTRPGKVKWLGEST 344  
 DB 241 SGAEVDACTWHYHLYNGRTATREDFLNPDVLDIFISSVQKVFQVVESTRPGKVKWLGEST 300  
 QY 345 SSAYGGGAPLSDTFAAGFMWLDKGLSARMGIEVWROVFPFNGKQVDKYLRLPLGPHGLSK 402  
 DB 301 SSAYGGGAGLSDTFVAGFMWLDKGLAATLGLVLRQVLIGAGSYHLDDNLDLPLRS 360  
 QY 403 -----DYWLSLFLKLVCTKVLMA-----SVQSGKRRKRLRVYLHCTNTD----- 442  
 DB 361 GLLLQDYWLSLFLKLVCTKVLMA-----SVQSGKRRKRLRVYLHCTNTD----- 418  
 QY 443 -----PRYKEGDLTLVAINLHNVTKLRLPYFPFNGKQVDKYLRLPLGPHGLSK 487  
 DB 419 QRKEARFSLVSLCSYRSGAATLMSMNLKQAPARISDPRILSSSTVEAFVLESQOP-GE 477  
 QY 488 LLSKSVQLNGLTKMVDQDTLPPLMEKPLRPGSSGLPAPFSYFVIRNAKVAACI 543  
 DB 478 LRSPAVKLVGRVLRWVDDDETFFPELEGRUPAAEHLQLPAYSLAFFVFTDAQAAGCV 533

## RESULT 11

Q9H37\_HUMAN  
 ID Q9H37\_HUMAN PRELIMINARY; PRT; 592 AA.  
 AC Q9H37;  
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE Hepatanase-like protein HPA2c.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea;  
 OC Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=2048345; PubMed=11027606; DOI=10.1006/bbrc.2000.3586;  
 RA McKenzie E., Smith P., Stamps A., Turner P., Barry R.,  
 RA Hircok M., Patel S., Barry E., Stubbelfield C., Terrett J., Page M.;  
 RT "Cloning and expression profiling of Hpa2, a novel mammalian

```
RT heparanase family member." ;
RL Biochem. Biophys. Res. Commun. 276:1170-1177(2000).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA McKenzie E.A., Tyson K., Stamps A.;
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF282887; AAG23423.1; -; mRNA.
DR GO; GO:0005622; C:intracellular; TAS.
DR GO; GO:0030305; F:heparanase activity; TAS.
DR InterPro; IPR005199; Glyco_hydro_79n.
DR Pfam; PF03662; Glyco_hydro_79n; 1.
SQ SEQUENCE 592 AA; 66580 MW; 95C384AD9A74258E CRC64;

Query Match 40.6%; Score 1154.5; DB 2; Length 592;
Best Local Similarity 43.6%; Pred. No. 1.7e-77;
Matches 250; Conservative 82; Mismatches 189; Indels 53; Gaps 9;

QY 20 PLGLPLSPGAL-----PRPA-----QAQDVVDLDPFTQEPHLHVSPPS 55
Db 18 PPACIAPGALYIALLLHLSLSQAGDRPLPVDRAAGLKEKTLILLDVSTKNPVRTVNE 77
QY 56 FLSVTIDANLATDPRFLILLGSPKRLTLARGLSPAYLRFGGTKTDFLIF----DPKKEST 111
Db 78 FLSLQLDPSIIHD-GWLDFLSSKRLVTLARGLSPAFLRFGGKRTDFLQFQNLNRPASRG 136
QY 112 FEERSYQSQVNQDI-----CKYGSIPDPVEEKLRLWPYQEQ-L-LREHYQK 158
Db 137 GPGPDYILKNVEDDIVRSDVALDKQKCKIAQ-HPDVMLEIQREKAAQMHLVLLKEQFSN 195
QY 159 KFKNSTYSRSSVDVLYTFANCSGLDLIFGLNALLRTADLQWNSNAQLLLDYCSSKGYN 218
Db 196 TYSNLIITARSLLKLYNFADCSGLHLIFALNALRRPNNSWNSSALSLLKYSAKKYNI 255
QY 219 SWELGNPNPSFKKADIFINGSQLGEDIYQLHKLRLK-STFKNAKLYGPDVQGPRRKTAK 277
Db 256 SWELGNPNRYRTMHEGRAVNGSQLGKDYIQLKSLQPIRIYSRASLYGNIGRPKNVIA 315
QY 278 MKSFLKAGGEVIDSVTHHYLYNGRTATREDFLNPVDLDFISSVQKVFQVVESTREGK 337
Db 316 LLDGFMKVAGSTVDVAVTWOHCYIDGRVVKVWDFLTKRLDLSQIRKIQKVNTYTPGK 375
QY 338 KVMIGETSSAYGGGAPLSDTFAAGFMWLDKLGLSARMGIEVWRQVFFGAGNTHLVDEN 397
Db 376 KIWLEGVYVTSAGGTTNLSDSYAAGFLWNLTLGMLANQIDVIRHSFFDGHYNHLVDQN 435
QY 398 FDPDPYWLSSLFKKLVGTGKVLMAVSQGSRR-----KLRYVLHCTNTNDNPKYKEG 448
Db 436 FNPLPDYWLSSLYKRLIGPKVLAVHVGAGLQKRPGRVIRDKLRIYARCTNHHNHNHYVRG 495
QY 449 DLTLYAINLHNVTYKLYRYPFSNKQVDKYLRLPLGPHGLLSKSVOLNGLTLKWVDDOTL 508
Db 496 SITUFIINLHRSRKIKLAGTLRDKLVHGYLLQPYGQGLSKSVQLNGQPLVMVDDGTL 555
QY 509 PPLMEKPLRPGSSGLPAFSYFFVIRNAKVAAC 542
Db 556 PELKPRPLRAGRTLVPVPTWGGFFVVKVNNALAC 589
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RESULT 12
Q5VUH6 HUMAN PRELIMINARY; PRT; 592 AA.
AC Q5VUH6;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Heparanase 2.
GN Homo sapiens (Human).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
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RP NUCLEOTIDE SEQUENCE.
RA Doggett S.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Holt K.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RA Pelan S.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
RN [4]
RP NUCLEOTIDE SEQUENCE.
RA Heath P.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
RN [5]
RP NUCLEOTIDE SEQUENCE.
RA Smith M.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL590036; CAH73137.1; -; Genomic DNA.
DR EMBL; AL39243; CA114146.1; -; Genomic DNA.
DR EMBL; AL356268; CAH70448.1; -; Genomic DNA.
DR EMBL; AL445251; CA116472.1; -; Genomic DNA.
DR EMBL; AL356220; CA117160.1; -; Genomic DNA.
DR EMBL; AL39243; CAH73137.1; JOINED; Genomic DNA.
DR EMBL; AL356220; CAH73137.1; JOINED; Genomic DNA.
DR EMBL; AL356288; CAH73137.1; JOINED; Genomic DNA.
DR EMBL; AL356268; CA114146.1; JOINED; Genomic DNA.
DR EMBL; AL445251; CA114146.1; JOINED; Genomic DNA.
DR EMBL; AL39243; CA117160.1; JOINED; Genomic DNA.
DR EMBL; AL590036; CA117160.1; JOINED; Genomic DNA.
DR EMBL; AL356220; CAH70448.1; JOINED; Genomic DNA.
DR EMBL; AL39243; CAH70448.1; JOINED; Genomic DNA.
DR EMBL; AL356268; CA116472.1; JOINED; Genomic DNA.
DR EMBL; AL356220; CA116472.1; JOINED; Genomic DNA.
DR EMBL; AL39243; CA116472.1; JOINED; Genomic DNA.
DR EMBL; AL445251; CA117160.1; JOINED; Genomic DNA.
DR EMBL; AL590036; CAH70448.1; JOINED; Genomic DNA.
DR EMBL; AL445251; CAH70448.1; JOINED; Genomic DNA.
DR EMBL; AL356268; CA117160.1; JOINED; Genomic DNA.
DR EMBL; AL590036; CA114146.1; JOINED; Genomic DNA.
DR EMBL; AL356220; CA114146.1; JOINED; Genomic DNA.
DR EMBL; AL445251; CAH73137.1; JOINED; Genomic DNA.
DR Ensemble; ENSG00000172987; Homo sapiens.
DR HGNC; HGNC:18374; HPSE2.
DR InterPro; IPR005199; Glyco_hydro_79n.
DR Pfam; PF03662; Glyco_hydro_79n; 1.
SQ SEQUENCE 592 AA; 66596 MW; 95C384AD9A6C868E CRC64;
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Query Match 40.5%; Score 1151.5; DB 2; Length 592;  
Best Local Similarity 43.4%; Pred. No. 2.9e-77;  
Matches 249; Conservative 83; Mismatches 189; Indels 53; Gaps 9;

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QY 20 PLGLPLSPGAL-----PRPA-----QAQDVVDLDPFTQEPHLHVSPPS 55
Db 18 PPACIAPGALYIALLLHLSLSQAGDRRPLPVDRAAGLKEKTLILLDVSTKNPVRTVNE 77
QY 56 FLSVTIDANLATDPRFLILLGSPKRLTLARGLSPAYLRFGGTKTDFLIF----DPKKEST 111
Db 78 FLSLQLDPSIIHD-GWLDFLSSKRLVTLARGLSPAFLRFGGKRTDFLQFQNLNRPASRG 136
QY 112 FEERSYQSQVNQDI-----CKYGSIPDPVEEKLRLWPYQEQ-L-LREHYQK 158
Db 137 GPGPDYILKNVEDDIVRSDVALDKQKCKIAQ-HPDVMLEIQREKAAQMHLVLLKEQFSN 195
QY 159 KFKNSTYSRSSVDVLYTFANCSGLDLIFGLNALLRTADLQWNSNAQLLLDYCSSKGYN 218
Db 196 TYSNLIITARSLLKLYNFADCSGLHLIFALNALRRPNNSWNSSALSLLKYSAKKYNI 255
QY 219 SWELGNPNPSFKKADIFINGSQLGEDIYQLHKLRLK-STFKNAKLYGPDVQGPRRKTAK 277
Db 256 SWELGNPNRYRTMHEGRAVNGSQLGKDYIQLKSLQPIRIYSRASLYGNIGRPKNVIA 315
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QY 3 LRSKPALPPMLLLGLPLSPGALPPRAQA-----QDVVDLDFFTQEPHLHLVSP 54
Db 16 LASLAALVP--LVUSSPYS--SSSTYQRPVAGKRPQGFVTRTLLDVNTRSFIRVND 71
QY 55 SFLSVTIDANLATDPRFLLILGSPKRLTLARGLSPAYLRFGGTKTDFLIFDPKKE----- 109
Db 72 NFLSLQLDPSIIKD-GWLDLFLSSGRVLTLARGLSPAFLRFGGKRTDFLQFTNQXNLAKFR 130
QY 110 ---STFEERSYQSQVNQDI-----CKYGSIPDPVEEKLRLWPYQEQ-L-LREHYQK 158
Db 131 GPGPDYLLKNYEDDIIRSDALDKQKCKLAS-HPDMMLELQREKAASQTQVLLKEQLSN 189
QY 159 KFKKST-----YSRS-----SDVLYTFANCGLDLIFGLNALLRTADLQWNSNAQLLLDY 210
Db 190 IYSNITLTGLFSHSRIARSLOKLYNFADCAHLLTLGNALHRPDPHSWNTSSTLSLUKY 249
QY 211 CSSKGYNISWELGNEPNSFLKADIFFINGSQGLGDIYQLHKLRLK-STFKNAKLYGPDVG 269
Db 250 SAGKYNISWELGNEPNAYRSMVGHAVNSSQLAQDYTKRLTLQSVRYYSRAQLYGNAG 309
QY 270 QPRKRTAKMLKSLFKAGGEVIDSVTHHHYLLNGRTATREDFLNPDVLDIFISSVQKVFQV 329
Db 310 RPRKNALLLDEFMKTGTGVVDAVTWQHYMDGRKKVEDFLKTRLLDTLQELSKVTKV 369
QY 330 VESTRPGKVMWLGTSSTAYGCGAPLSDTEAAGFMWLDKGLSARMGLEVVVR-----QVF 385
Db 370 VNTHTPGKVMWLGGLPWTGMSNLSDTFAGFLVWNTLGMWAOQIDVVRQAVQEH 429
QY 386 FGAGNYHLVDENFDP-LPDYMLSLFLFKLVGTVKVLMAVQSGSKR-----KLRYVL 435
Db 430 TNKQSVLFLQMFVPSFPDYFSLVFLKVLAVRVAGLQRPQGRVIRDKLRIYA 489
QY 436 HCTNTDNPYKEGDLTLYAINLHNVTYKRLPYPPSNQVDKYLRLRPLGPHGLLSKVQL 495
Db 490 HCTSYSNHNRYRGSITIIILNHSRKKIKLAGTLRNINIVHQYLLQPYGADGLAKHVQL 549
QY 496 NGLTLKMVDDOTLPLMEKPLRPQSSGLGPAFSYFFVIRNAKYAAC 542
Db 550 NGEKLLMADNETFPELKPRTLRAAGRTIAMPPMTIGFYVIRKINAYAC 596

RESULT 15
Q5VUH4 HUMAN PRELIMINARY; PRT; 548 AA.
ID Q5VUH4;
AC Q5VUH4;
DT 01-FEB-2005 (TReMBLrel. 29, Created)
DT 01-FEB-2005 (TReMBLrel. 29, Last sequence update)
DT 13-SEP-2005 (TReMBLrel. 31, Last annotation update)
DE Heparanase 2
GN Name=HFE2; ORFNames=RP11-439D8.2-002;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Doggett S.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Holt K.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RA Pelan S.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
RN [4]
RP NUCLEOTIDE SEQUENCE.
RA Heath P.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
RN [5]
RP NUCLEOTIDE SEQUENCE.
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Smith M.;
RA Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
RL EMBL; AL590036; CAH73139.1; -; Genomic_DNA.
DR EMBL; AL356220; CAH17162.1; -; Genomic_DNA.
DR EMBL; AL356268; CAH70450.1; -; Genomic_DNA.
DR EMBL; AL445251; CAH16474.1; -; Genomic_DNA.
DR EMBL; AL139243; CAH14148.1; -; Genomic_DNA.
DR EMBL; AL139243; CAH73139.1; JOINED; Genomic_DNA.
DR EMBL; AL356220; CAH73139.1; JOINED; Genomic_DNA.
DR EMBL; AL445251; CAH73139.1; JOINED; Genomic_DNA.
DR EMBL; AL356220; CAH14148.1; JOINED; Genomic_DNA.
DR EMBL; AL445251; CAH17162.1; JOINED; Genomic_DNA.
DR EMBL; AL356268; CAH17162.1; JOINED; Genomic_DNA.
DR EMBL; AL356220; CAH17162.1; JOINED; Genomic_DNA.
DR EMBL; AL445251; CAH70450.1; JOINED; Genomic_DNA.
DR EMBL; AL356220; CAH70450.1; JOINED; Genomic_DNA.
DR EMBL; AL39243; CAH70450.1; JOINED; Genomic_DNA.
DR EMBL; AL39243; CAH16474.1; JOINED; Genomic_DNA.
DR EMBL; AL356268; CAH16474.1; JOINED; Genomic_DNA.
DR EMBL; AL39243; CAH16474.1; JOINED; Genomic_DNA.
DR EMBL; AL39243; CAH16474.1; JOINED; Genomic_DNA.
DR EMBL; AL590036; CAH14148.1; JOINED; Genomic_DNA.
DR EMBL; AL356268; CAH14148.1; JOINED; Genomic_DNA.
DR EMBL; AL356288; CAH73139.1; JOINED; Genomic_DNA.
DR InterPro; IPR005199; Glyco_hydro_79_N.
DR Pfam; PF03662; Glyco_hydro_79n; 1.
SQ SEQUENCE 548 AA; 61816 MW; 2572C68423CD2C51 CRC64;

Query Match 35.9%; Score 1021.5; DB 2; Length 548;
Best Local Similarity 42.6%; Pred. No. 1.4e-67; Indels 53; Gaps 9;
Matches 223; Conservative 77; Mismatches 171;

QY 20 PLGLPLSPGAL-----PRPA-----QAQVVVDLDFFTQEPHLHLVSPS 55
Db 18 PPACIAPGALYALALLHLSSQAGDRRLPVDRAAGLKEKTLILLDVSTKNPVTNVEN 77
QY 56 FLSTVIDANLATDPRFLLILGSPKRLTLARGLSPAYLRFGGTKTDFLIF-----DPKKEST 111
Db 78 FLSLQLDPSIITHD-GWLDLFLSSKRLVTLARGLSPAFLRFGGKRTDFLQFQNLNRPASRG 136
QY 112 FEERSYQSQVNQDI-----CKYGSIPDPVEEKLRLWPYQEQ-L-LREHYQK 158
Db 137 GPGPDYLLKNYEDDIVRSDVALDKQKCKIAQ-HPDVMLELQREKAAGHLVLLKEQFSN 195
QY 159 KFKNSTYSRSSVDVLYTFANCGLDLIFGLNALLRTADLQWNSNAQLLLDYCSSKGYNI 218
Db 196 TYSNLIITARSUDKLYNFADCSGLHLIFALNALRPNNSWSSSALLKYSASKYNI 255
QY 219 SWELGNPNSFLKKADIFINGSQGLGDIYQLHKLRLK-STFKNAKLYGPDVQGPQRKTAK 277
Db 256 SWELGNPNNYRTMHWGRAVNGSLGKDYIQLKLLQPIRIYSRASLYGPNIGRPRKNVIA 315
QY 278 MKSFLKAGGEVIDSVTHHHYLLNGRTATREDFLNPDVLDIFISSVQKVFQVVESTRGK 337
Db 316 LLDGFMKVAGSTVDAVTWQHCHYIDGRVVVKVMDFLKTRLLDLSQIRKIQKVNTYTPGK 375
QY 338 KVLGGETSSAYGCGAPLISDTFAAGFMWLDKGLSARMGLEVVVRQVFFGAGNYHLVDEN 397
Db 376 KIWLEGVVTTAGGTNNLSDSYAAGFLWNLTLGMLANQIDVIRHSFFDHGNYHLVDQN 435
QY 398 FDLPLDYWLSLLFKKLVGTVKVLMAVQSGSKR-----KLRYLHCTNTDNPYKEG 448
Db 436 FNPLPDYWLSLLYKRLIGPKVLAVHAGLQRPGRVIRDKLRIYACTNNHNNYVRG 495
QY 449 DLTLYAINLHNVTYKRLPYPPSNQVDKYLRLRPLGPHGLLSKS 492
Db 496 SITLFIINLHRSRKKIKLAGTLRDKLVHQYLLQPYGQEGLSKST 539

Search completed: February 27, 2006, 17:38:45
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Job time : 237 secs

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GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on: February 27, 2006, 17:35:01 ; Search time 41 Seconds  
(without alignments)  
1274.285 Million cell updates/sec

Title: US-10-676-079-2  
Perfect score: 2842  
Sequence: 1 MLRSKPALPPPLMLLLGP.....LPAPSYFFVIRNAKVAACI 543  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues  
Total number of hits satisfying chosen parameters: 283416  
Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_80.\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	897.5	31.6	480	2 JC7506	heparanase protein
2	416	14.6	521	2 T45608	hypothetical prote
3	169.5	6.0	190	2 T01953	hypothetical prote
4	112.5	4.0	356	2 F64383	hypothetical prote
5	111.5	3.9	575	2 T12094	beta-fructofuranos
6	111	3.9	670	2 T10666	hypothetical prote
7	111	3.9	688	2 S32961	hypothetical prote
8	111	3.9	2298	2 T49648	hypothetical prote
9	109.5	3.9	879	2 E91031	probable outer mem
10	108.5	3.8	411	2 S74760	hypothetical prote
11	107.5	3.8	500	2 D87541	beta-xylosidase [i
12	106	3.7	879	2 F85875	probable fibrinoly
13	105	3.7	670	2 T38446	microtubule-associ
14	104.5	3.7	788	1 S00652	phosphoribosylamin
15	104	3.7	432	2 F70411	adenylosuccinate s
16	104	3.7	2013	2 A11489	probable peptidogl
17	103.5	3.6	587	2 S36231	beta-fructofuranos
18	103.5	3.6	676	2 AF1153	transcription anti
19	103.5	3.6	687	2 F85188	retrotransposon li
20	103	3.6	796	2 D97065	transketolase (imp
21	101	3.6	594	2 A82913	hypothetical prote
22	101	3.6	644	2 A97268	methionyl-trna syn
23	100.5	3.5	805	2 C86525	DNA gyrase subunit
24	100.5	3.5	805	2 H72098	DNA gyrase, chain
25	100.5	3.5	989	2 A82140	toxin secretion AB
26	99.5	3.5	510	2 H69893	conserved hypothet
27	99.5	3.5	837	1 A31842	endo-1,4-beta-xyla
28	99	3.5	897	2 G02529	dynein heavy chain
29	99	3.5	4644	1 A38905	dynein heavy chain

30 98.5 3.5 596 2 T04506  
31 98.5 3.5 629 2 C64180  
32 98.5 3.5 654 2 T14202  
33 98.5 3.5 699 2 F95146  
34 98.5 3.5 701 2 D98014  
35 98.5 3.5 746 2 T46821  
36 98.5 3.5 746 2 A95420  
37 98.5 3.5 1012 2 JC5925  
38 98 3.4 465 2 T19113  
39 98 3.4 716 1 C60008  
40 98 3.4 760 2 T34414  
41 98 3.4 817 2 H75035  
42 97.5 3.4 454 2 T20829  
43 97.5 3.4 511 2 S61166  
44 97.5 3.4 604 2 E75119  
45 97.5 3.4 804 2 G71546

ALIGNMENTS

RESULT 1

JC7506  
heparanase protein 2a - human  
C:Species: Homo sapiens (man)  
C:Date: 17-Nov-2000 #sequence\_revision 17-Nov-2000 #text\_change 09-Jul-2004  
C:Accession: JC7506  
R:McKenzie, E.; Tyson, K.; Stamps, A.; Smith, P.; Turner, P.; Barry, R.; Hirccock, M.; i  
Biochem. Biophys. Res. Commun. 276, 1170-1177, 2000  
A:Title: Cloning and expression profiling of Hpa2, a novel mammalian heparanase family  
A:Reference number: JC7506  
A:Accession: JC7506  
A:Molecule type: mRNA  
A:Residues: 1-480 <MCK>  
A:Cross-references: UNIPROT:Q9HB39; UNIPARC:UPI000003888A; GB:AF282885  
C:Comment: This protein, an intracellular membrane-bound enzyme, has biological and the  
therapies.  
C:Genetics:  
A:Gene: hpa2a  
A:Map position: 10q23-10q24  
C:Keywords: heparin binding; membrane bound

Query Match 31.6%; Score 897.5; DB 2; Length 480;  
Best Local Similarity 36.0%; Pred. No. 5.5e-59;  
Matches 202; Conservative 74; Mismatches 146; Indels 139; Gaps 9;  
Qy 20 PLGLSPGAL-----PRPA-----QAQDVVDLDFFTQEPHLNPS 55  
Db 18 PPACAPGALYLALLHLSSQAGDRRPLFVDRAAGLKEKTLILLDVSTKNPVRTV 77  
Qy 56 FLSVTIDANLATDPRFLILGSPKRLTLARGLSPAYLRFPGTKTDFLIF----DPKKEST 111  
Db 78 FLSQLDPSIHD-GWLDFFLSKKELVTLARGLSAPLRFPGTKRTDFLQFQNLRPASR- 135  
Qy 112 FEERSYQSQVNQDICKYISPPDVEKLEWMPYQBSQLLREHYKKFNSTYSRSVD 171  
Db 136 -----CGFGPD-----YLLKNYE----- 148  
Qy 172 VLYTFANCSDLIFGLNALLRTADLQWSSNAQLLLDYCSSKGYNISWELGNPNSFLK 231  
Db 149 -----DEPNRYT 156  
Qy 232 KADIFINGSQGLGDIYQLHLLRK-STFKNAKLYGPDVGOPRRKTKAMKLSFLKAGEVI 290  
Db 157 MGRVAVNGSQLGDIYQLKSLQIPRIYSRSLYGNIGRPRKNVIALLDGFMKVGSTV 216  
Qy 291 DSVTWHYYLNGRTATREDFLNPDVLDIFISSQVKVFQVVESTRPGKKVWLGETSSAYGG 350  
Db 217 DAVTWQHCYIDGRVWKVMDFLKTRLLDLSQIRKIQKVNTYTPGKKIWLEGVVTTTSG 276  
Qy 351 GAPLLSTPFAAGFWLKDGLSARMGIEVVMRQVFFGAGNYHLVDENFDPLDPYWLSLFP 410  
Db 277 GTNNLSDSYAAGFLWNLTLGLMLANQIGIDVIRHSFFDHGYNHLVDQNFNPLDPYWL 336





```
Db      |   :   :   |   |   :   :   |  
506 GNNKKLSLRSL-----IDHSVSVESFGVGSKT 531  
  
RESULT 6  
Tl0666  
Hypothetical protein FE21.40 - Arabidopsis thaliana  
C;Species: Arabidopsis thaliana (mouse-ear cress)  
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #te:  
C;Accession: Tl0666  
R;Bevan, M.; Lennard, N.; Quail, M.; Harris, B.; Rajan  
submitted to the Protein Sequence Database, June 1999  
A;Reference number: Z16533  
A;Accession: Tl0666  
A;Molecule type: DNA  
A;Residues: 1-670 <BEV>  
A;Cross-references: UNIPROT:Q9M090; UNIPARC:UPI00000A44  
A;Experimental source: cultivar Columbia; BAC clone F6  
C;Genetics:  
A;Gene: ATSP:F6E21.40  
A;Map position: 4  
A;Introns: 47/3; 87/1; 123/3; 203/3; 230/2; 255/3; 284/  
C;Superfamily: Schizosaccharomyces pombe negative regu
```

Query Match	3.9%;	Score 111;	DB 2;	Length 670;
Best Local Similarity	22.4%;	Pred. NO. 3.6;		
Matches 123;	Conservative 77;	Mismatches 194;	Indels 156;	Gaps 33;
Qy	51	LVSFSLVSTVDIANLATDPRFLTLGSGPKLRTLARGLSPAY--LRFGGTKTDFLFDPK--	107	
Db	47	LVDPSRPSLVEGN-GVDTQVLPCVGSDLV-----LSPQSSSHVVGVKISSWLLDSDS	99	
Qy	108	-----KSTFFERSYMQVQNOQDICKYSGISIPDVEEKLRLWPYEQILLRHHYQKKFK	161	
Db	100	EVLRMDSETFLKQEIATWATHLSQMC-----PD-----LTRPHYLAGGL	139	
Qy	162	NSTYSRSSV-----DVLV-----TFANCS--GLDLIFCLNALRLTABLQWNSSNAQLL	207	
Db	140	RVSCCRSSFTSDTFYKITFQNALTFCGSSLPCLNVSALKLWLRLVPLVK-----SEGDSM	196	
Qy	208	LDYCSSKGVNYSWELGN-----EPNSFLKKA-DIFIN-----CSQSGEDIQLHKLL	253	
Db	197	DD--TSEGNDNSWELNNSFLFLCEHDSKLSVALDVLTSPSETSLGRWNGES--VRAIILS	253	
Qy	254	RKSTFTKNAKLYGPDVGQP--RRKTAKMLKSFL-KAGGEVIDSVTWHYYLNGRTATREDF	310	
Db	254	TDAFLTNAR-----GYPLCKSRKHOKLIAGFFPDHAQOVVICGKPVNLQKPLDSSSEGTE	307	

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Qy      311 LNPDLVDLFISSVQKVFQVVESTPRGKKYVMWGTSAYGGGAPLLSDTFAAGFMWLDKLG   370
       |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      308 KNP--LRIVLDYVAYLFQKMESLSEQRTELGVGRDFLQAPLQPLMDNLEAQTVTETFE--- 362
       |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Qy      371 LSARMGIEVMRQVFFGAGNYHLVDENFDPDLYWLSSLFKKLVGTKVLK----- 420
       |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      363 ----RDSVKIIOYQ----RAVEKALVDR---VPDEKASEL-----TTVLMMVGAGRGLV   406
       |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Qy      421 -ASVQGSKR-RKRLRVYLCTNTNDNPRYKEGDITLVAINLNHTK-----YYLRLPY   468
       |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      407 RASLQAARETDRLKLY----AVEKNPN-----AVTLHNLVKGMEHDVVTIISCDM   455
       |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Qy      469 PFNSN--KQVDKYLLRPGLPHGLLSKSVQLNGLTLMKVDDQTUPLPM---EKLPRGSSLG   523
       |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      456 RFWNAPEQADILVSELGSGFG-----DNELSPEDLGARFLKP-DGIS   498
       |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Qy      524 LPAFSYSFFV   533
       |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      499 IPS-SYTSEI   507
       |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||

RESULT 7
S32961
hypothetical protein YBR259w - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein YBR1727

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hypothetical protein YBR259W - yeast (Saccharomyces cerevisiae)  
S32961  
N:Alternate names: hypothetical protein YBR1727

C;Species: Saccharomyces cerevisiae  
C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 09-Jul-2004  
C;Accession: S32961; S46140  
R;Doignon, F.; Biteau, N.; Crouzet, M.; Aigle, M.  
Yeast 9, 189-199, 1993  
A;Title: The complete sequence of a 19,482 bp segment located on the right arm of chromosome 10.  
A;Reference number: S29348; MUID:93220397; PMID:8465606  
A;Accession: S32961  
A;Status: translation not shown  
A;Molecule type: DNA  
A;Residues: 1-688 <DOI>  
A;Cross-references: UNIPROT:P38338; UNIPARC:UPI000013A298; EMBL:X70529; NID:g1907246; PIR:R00001  
R;Aigle, M.; Baclst, M.C.; Barthe, C.; Biteau, N.; Crouzet, M.; Doignon, F.  
submitted to the Protein Sequence Database, August 1994  
A;Reference number: S45940  
A;Accession: S46140  
A;Molecule type: DNA  
A;Residues: 1-688 <ATG>  
A;Cross-references: UNIPARC:UPI000013A298; EMBL:Z36128; NID:g536684; PIDN:CAA85222.1; PIR:R00001  
C;Genetics:  
A;Cross-references: SGD:S0000463  
A;Map position: 2R  
C;Superfamily: Saccharomyces cerevisiae hypothetical protein YBR259w

Query Match 3.9%; Score 111; DB 2; Length 688;  
Best Local Similarity 22.5%; Pred. No. 3.7;  
Matches 67; Conservative 45; Mismatches 94; Indels 92; Gaps 16;

Qy 126 ICKYGSIPPDVEEKLRLWEPYQEOQLLREHYQKFKNSYSSRS-----VDVLYT 175  
Db 164 MAEYSSKWDSDKQLOFMFEYFKMLKECLVYENFDLQKSDPLKELIIPWEKIVYV 223

Qy 176 FANGSGDLIFGLNALLATDQWNSN-----AQLLD-----YCCKGY----- 216  
Db 224 -ANC--IDAFTGEQVRIDGAEIWTSKNLVFSSISSAVRLNDLQNMFSAPRYGEEALV 280

Qy 217 -----NISWELGNEPNSFLKKA---DIF--INGSQLG--EDYIQLHKLARK----- 255  
Db 281 QDFAHRSKWDSDNDKVESLRALIFNDMFYFNKEQVDTKADGFIFFLRLLRKNFKEHIN 340

Qy 256 -----STFKN--AKLYGPDVGQPRRTAKMLKSLFKAGGEV-----IDSV 293  
Db 341 DVKDFHIOVIKYLNSQFNKYSTLMTSSKTQDRKSHNMPSILLDDGNKIGHVSPIDE- 399

Qy 294 TWHYYLNG-----RTATREDFLNPDLIFISSVQKVFQVVESTR---PGKK 338  
Db 400 -YSHFIDNDEPLWRDKVYPKIYTNBQTPDASAIFDS--HKIVAIISLLRYLYLPEKR 454

RESULT 8  
T49648  
hypothetical protein B8B20.20 [imported] - Neurospora crassa  
C;Species: Neurospora crassa  
C;Date: 02-Jun-2000 #sequence\_revision 02-Jun-2000 #text\_change 09-Jul-2004  
C;Accession: T49648  
R;Schultze, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura, F.  
submitted to the Protein Sequence Database, May 2000  
A;Reference number: Z25022  
A;Accession: T49648  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-2298 <SCH>  
A;Cross-references: UNIPROT:Q96U00; UNIPARC:UPI000017B4BA; EMBL:AL355933; GSPDB:GN00116;  
A;Experimental source: BAC clone B8B20; strain OR74A  
C;Genetics:  
A;Gene: NCSP:B8B20.20  
A;Map position: 6  
A;Introns: 426/3

Query Match 3.9%; Score 111; DB 2; Length 2298;  
Best Local Similarity 19.3%; Pred. No. 23;  
Matches 114; Conservative 79; Mismatches 190; Indels 208; Gaps 28;

Qy 78 PKLRTTLARGLSA-----YLRFGTGTDFLIDPDKKSTPEERSYQWOSQV-NODIC 127  
Db 1447 PRVDLIERLITPSNAHKEACLINIRANQLARLVVSNVSGEGSASFRPITWRNNVFNQILD 1506

Qy 128 KYGSIPPDVEEKLRLWEPYQEOQLLREHYQKFKNSYSSRSVDVLYTTPAN 178  
Db 1507 QYMSAESDIEQOFRALSAENMRSIDAAWRELIITKN-----KATALDILHTSAR 1555

Qy 179 CSGLDLIFGLNAL-----LRTADLQ-----WNSSNAQLLLDYCSSKGNYI 218  
Db 1556 AS-LDVLKQAKTLEAAIYVTLNVTLOQKMTCTTLHFGSPGFDWGILNVAL-----DTHAHFL 1609

Qy 219 SW-ELGNEPNSFLKADIFINGSOLGEDYIQLHKLARKSTFKNAKLYGPDVGQPRRKTA 277  
Db 1610 GWIETSEEQYSSNESSADIDPROLEDAILLQKLTKKEFFWMA-----RELLAL 1659

Qy 278 MLKSLFKAGGEVID-SVTWTHHYLNGRTATREDFLNPDLIFISSVQKVFQVVESTRPG 336  
Db 1660 PLKAITTFGKTEQOVACTEKTIVTLAAKLAAR-----FIQ--ERVTVQLPYFPQG 1706

Qy 337 K-----KWLGETSSAYGGGAPLLSDTFAAG-----FMWLDK 368  
Db 1707 KYGLFPDMPKMGSPERRWL-----PLFIATLVNKNVDFDKDIETNLSLWQS 1755

Qy 369 LGLSAR-MGIEVVMROVFFGAGNVHL--VDSENPDLDPDYWLSL-LFKKLVG--TKVL-- 419  
Db 1756 IIKPMRFLGYETYLAEVLQQRGLFLAEADVAGMTPDYINHLDFSRAIHYMRKALRGG 1815

Qy 420 -----MASVQSGK-----RRKLRYVLHCTNTDNPRYKEGDLTLVAINLHNVTXYL 464  
Db 1816 ATTPAGVTSSASTAGSSSAQSIRQRREFSH----- 1847

Qy 465 RLPYFPFNKQVDKYLRLPLG-----PHGLLSKSVQLNGLTLMXVD-- 504  
Db 1848 TLQAMTNIKXDLFLRLSLALADPTASSTEEHRDYMAFTGLIS-LIKSHGVGIVVDSF 1906

Qy 505 -----DQTLPLMEKPLRPG-----SSLGLPAPSYSF-FVIRNAKVA 540  
Db 1907 FLTPDSYSPPLOPQPLQTAGIMAYGVRLSEKDVPAASQLFWYLFNNFKVA 1957

RESULT 9  
E91031  
probable outer membrane protein ECs3221 [imported] - Escherichia coli (strain O157:H7, serotype O157)  
C;Species: Escherichia coli  
C;Date: 18-Jul-2001 #sequence\_revision 18-Jul-2001 #text\_change 05-Oct-2004  
C;Accession: E91031  
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.  
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.  
DNA Res. 8, 11-22, 2001  
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genomic maps of the enterohemorrhagic Escherichia coli O157:H7 and enterohemorrhagic Escherichia coli O157:H7  
A;Reference number: A99629; MUID:21156231; PMID:11258796  
A;Accession: E91031  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-879 <HAY>  
A;Cross-references: UNIPROT:Q8XCP4; UNIPARC:UPI00000D0453; GB:BA000007; PIDN:BA036644.1;  
A;Experimental source: strain O157:H7, substrain RIMD 0509952  
C;Genetics:  
A;Gene: ECs3221  
C;Superfamily: outer membrane usher protein fimD

Query Match 3.9%; Score 109.5; DB 2; Length 879;  
Best Local Similarity 20.1%; Pred. No. 7;  
Matches 130; Conservative 68; Mismatches 208; Indels 241; Gaps 33;

Qy 52 VSPFLSVITDANLATDPRFLILGSPKLRTLARGLSPAYLRFSGTKTDFLIDFKKEST 111  
Db 20 MSGSYNAWAENEIQFDSRFLKGDTKI-DLKRFPSSQGYVEPG--KYNLQQLNKKQPLT 76

Qy 112 FEERSYQWOSQVNDICKYGSIPPDVEEKL-----RLEWYQEQQLLREHYQKFKNS 163  
Db 77 EYDIYWAASENDASKTYACLTPELVAQFGLKEDVAKNLQWHDGKCLKPGGLE----- 130

Qy	164	TYSRSDVLYTFANCSGLDLIFGL-NALLRTADLQWNSN-----AQLLDYC-----	211
Db	131	-----GIDIK-----ADLSQALVISLPOAYLEYTDINWDPSPWDDGISLIADYSITAQ	182
Qy	212	-----SSKGYNI-SWEEL-GNEPNSFL-----KKADIFINGSQ-----	241
Db	183	RHEENGDDSNESISNGTGVGNVLGAWRLRADWQTDYLHKSNDVDDVINGDDTDQKNWWSR	242
Qy	242	-----LGEDYIQLHLRLKRSTF-----KNAKLYGPDV	268
Db	243	YYAWRALPSLKAUKLGGEDY-----LNSDIFDGFNYVGGISITDDQMLPPNLRGYAPDI	296
Qy	269	GOPRRKTAAMLKGFUKAGEVI-----DSVTWHHYLNGRTATREDFLN	312
Db	297	SGVAHTTAKVTVSQL-----GRVIYETQVPAGPPRIQDLGDSV-----SGTLHRIIEQN	346
Qy	313	PDVLDDIFISSVQKVQVVESTPGK-----KWML-----GETS-----	345
Db	347	GOVQEYDINTASMPF-----LTRPGQVRYKLMGRPQEWGHHVEGGFFSGGEASGIANGW	402
Qy	346	SAYGGGAPLLSD-----YFAA-----GFMMLDKL-----GLSAR	374
Db	403	SLYGEA-----LADEHYQSAALGVGRDLSVFGAVAFDITSHSTRKLDKETAYKGGSLDGN	459
Qy	375	MGI-----EVVMQVFFGAGNVLVDENFDPLPDYWLILLFKKLVTG---KVLMAVQGS	426
Db	460	LSYSKDPDELNSRVTFAG---YRFSEENFMTWSEY-LDASDEWVRTGDKEMYTATVNO	515
Qy	427	KRRKLRYVLHCTNTDNPYKEGDLTYAI-----NLHNVTK-----	462
Db	516	NFRDAGSVLYNLNYTRHTYWRDREQTYNVMLSHYFNLSIRNWSISMTGYRYEYDNOQDK	575
Qy	463	---YLRLPYFPFNKQVDKYLRLPGLBPHGLLSKSVQLNGLTLKMWDDQT	507
Db	576	GWYISLSMPWGDSSSTISY-----NGNYGSGSDSSQVG---YFRSRVDDAT	616

RESULT 10  
S74760  
hypothetical protein slr1617 - *Synechocystis* sp. (strain PCC 6803)  
C:Species: *Synechocystis* sp.  
A:Variety: PCC 6803  
C:Date: 25-Apr-1997 #sequence\_revision 25-Apr-1997 #text\_change 09-Jul-2004  
C:Accession: S74760  
R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;  
O. K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda  
DNA Res. 3, 109-136, 1996  
A:Title: Sequence analysis of the genome of the unicellular cyanobacterium *Synechocystis*  
s.  
A:Reference number: S74322; MUID:97061201; PMID:8905231  
A:Accession: S74760  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-411 <KAN>  
A:Cross-references: UNIPROT:P72895; UNIPARC:UPI00000C0C3B; EMBL:D90901; GB:AB001339; NIT  
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

Query Match	3.8%;	Score 108.5;	DB 2;	Length 411;
Best Local Similarity	21.4%;	Pred. No. 2.6;		
Matches	66;	Conservative 55;	Mismatches 94;	Indels 93; Gaps 17;
Qy	159	KFKNSTYRSRSDVLYTFANCSGDLDF--GLNALLRTADLWNSSNAQL-----	206	
Db	151	EFRUISPTREQIDF---FAGSTKLDLLASENIDICVHLANPRVYTSNVANGQTULTMURN	207	
Qy	207	LLDYCSSKG---YNISMEL-----GNEPNSFLKK-----ADIFINGSOLGE	244	
Db	208	VIDVCLAKDIPLIYPSSEWYISGVAGTHADESPALPRGPYGETKYLAELI-----	260	
Qy	245	DYIQLHLLRRKSTFPKNAKLYGPDVCGQPRRTAKMLKSLFAGGGEVIDSVTWHHYNLNGRT	304	
Db	261	DHCRRTGLRCAILLRSPVYSGMSDKP-----KPIFNFKKASOGKIVT---HHYING--	311	

[illegible]

## RESULT 11

D87541  
beta-xylosidase [imported] - Caulobacter crescentus  
C:Species: Caulobacter crescentus  
C:Date: 20-Apr-2001 #sequence\_revision 20-Apr-2001 #text\_change 09-Jul-2004  
C:Accession: D87541  
B:Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, R.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Koln, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.I. Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001  
A:Title: Complete Genome Sequence of *Caulobacter crescentus*.  
A:Reference number: A87249; MUID:21173698; PMID:11259647  
A:Accession: D87541  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-500 <STO>  
A:Cross-references: UNIPROT:Q9A5U0; UNIPARC:UPI00000C76D1; GB:AE005673; NID:g13423886;  
C:Genetics:  
A:Gene: CC2357

Query Match	3.8%	Score 107.5;	DB 2;	Length 500;
Best Local Similarity	25.7%;	Pred. No. 4.2;		
Matches	56;	Conservative	80;	Indels 47;
		Mismatches	35;	Gaps 15;

Qy	165	YSRSSVDVLYTFANCGLDLIFGLN---	ALLRTAD---	LOW--NSSNAQL-----	LLD---	209
Db	81	YDWTKDQLDYALLAKGIPKPIELGFTPEAKMTSDQITFYKWKNTSHPKLGPWRDLIDAP	140			
Qy	210	-YCSSKGYNI-----	SW--ELGNEN--	SPLKADIFINGSQLGEDYIQLHLLRSTFFGN	260	
Db	141	VHHLRARYGVEEVRTWTFEYVNEENLDGFWEKAD-----	QAAAFELYDV---	TARA	188	
Qy	261	AKLYGPD--	VQOPRRKTKAMLKSPF---	KAGEVIDSVTWHYYLNG-----	RTATREDFL	311
Db	189	IKAIDPSLRVGGPATAGAAWPEFLAHVKKSSAVDFVTTHTYGYDGGFLDEKGVQDTKL	248			
Qy	312	NPVDLDIFISQVKVQFQVVE--	STRPGKKVWLGETSSAY	348		
Db	249	SPSP-DAWGDVRRVRREQIIBASAPFGLPYFTWSTSY	285			

## RESULT 12

F85875  
probable fimbrial usher Z3600 [imported] - Escherichia coli (strain O157:H7, substrain  
C;Species: Escherichia coli  
C;Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 05-Oct-2004  
C;Accession: F85875  
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew  
iller, L.; Grobbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca  
Nature 409, 529-533, 2001  
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.  
A;Reference number: A85480; MUID:21074935; PMID:11206551  
A;Accession: F85875  
A;Status: Preliminary  
A;Molecule type: DNA  
A;Residues: 1-879 <STO>  
A;Cross-references: UNIPROT:Q8XCP4; UNIPARC:UPI000016598B; GB:AE005174; NID:g12516702;  
A;Experimental source: strain O157:H7, substrain EDL933  
C;Genetics:



A;Experimental source: strain 972h-; cosmid c405

C;Genetics:

A;Gene: ADE1; SPDB:SPBC405.01

A;Map position: 2

C;Superfamily: Saccharomyces cerevisiae ADE5 multifunctional protein; phosphoribosylamin

C;Keywords: cyclo-ligase; purine nucleotide biosynthesis

F;5-425/Domain: phosphoribosylamine-glycine ligase homology <PGL>

F;439-767/Domain: phosphoribosylformylglycinamide cyclo-ligase homology <PFCL>

Query Match 3.7%; Score 104.5; DB 1; Length 788;

Best Local Similarity 27.7%; Pred. No. 14;

Matches 70; Conservative 36; Mismatches 114; Indels 33; Gaps 11;

Qy 297 HYLYNGRTATRE--DFLNPV-LDIFISSVQKVFQVVEST-RPGKVKVLGETSSAY---- 348

Db 424 HHALNPKRKTRITLYENSGVSVVDNEFVQRIKDLVKSTRPGADADIGGFGGIPDLK 483

Qy 349 -GGGAPLL-SDTFAAGFWMLDKGLSAR--MGIEVMRQVFPFGAGNTHLVDFNFDPL--P 402

Db 484 AGMNDPLLVSATDGVGSKLLTALSINKHDTVGIDLVAMNV-----NDLVVQGAEPILFL 537

Qy 403 DYWLSLLFKLVGKVLMAVQSGSKRKLRYLHCTNTDNPYKKEGDLTLVAINLHNVTK 462

Db 538 DYFATGSLDLKYSTFVEGVVKGCKQACALVGGETSEMPGLYHDGDANGTSVGAVSR 597

Qy 463 YLRLPYPFSNKKVDKYLRLPLGPHGLLSKVSQNLGLTL--KMVD---DQTLPLMEKPL 516

Db 598 DDILPKPESFSGDILL-----GLASDGVHSGYSLVRKIVEYSDLEVTSCPMDKNV 650

Qy 517 RPSGSLGLPAFSY 529

Db 651 RLGDLLIPRIY 663

RESULT 15

F70411

adenylosuccinate synthetase - Aquifex aeolicus

C;Species: Aquifex aeolicus

C;Date: 08-May-1998 #sequence\_revision 08-May-1998 #text\_change 09-Jul-2004

C;Accession: F70411

R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; O

V.

Nature 392, 353-358, 1998

A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.

A;Reference number: A70300; MUID:98196666; PMID:9537320

A;Accession: F70411

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-432 <AQF>

A;Cross-references: UNIPROT:O67321; UNIPARC:UPI00000565A2; GB:AE000733; NID:g2983720; P

A;Experimental source: strain VF5

C;Genetics:

A;Gene: pura

C;Superfamily: adenylosuccinate synthase

Query Match 3.7%; Score 104; DB 2; Length 432;

Best Local Similarity 23.9%; Pred. No. 6.1;

Matches 96; Conservative 39; Mismatches 128; Indels 138; Gaps 22;

Qy 15 LLLGLPLGSPGALPPAQADQVVDLD-----FFTQEPHLHLYSPS 55

Db 51 ILHLLPTGILHEHVKGVIAGM-VVDLEVLHKEVKLEEKGIYVKERLIFISDRAHLVMPY 109

Qy 56 FLSVTIDANLATDFRLLILGSPK--LRTLARGLSPAYL-RFGGKTGDFLIFDPKKESTF 112

Db 110 H-----KLLDSLFEKKKGIGTTLRGIGPAYMPKYG--RKGIRISDLKDKRF 154

Qy 113 EERSYWSQVNODICKYGSIPPDVEEK-----LRLEWPYOEOLLRHVKQKFKNSTY 165

Db 155 ----YTLLEDNLDVFK-----NICEKVFCEKFDLDINOIYEEQL-----RYFEFKENV- 199

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Qy 222 LGNEPNSFLKKADIFING-----SQL-GEDYIQLHKLRLKSTFKNAKLYG 265

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Db 344 YELDGEVIDYFPASYSELIRKVPYKTLKG---WKKSTKGA 381

Search completed: February 27, 2006, 17:39:32

Job time : 44 secs

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GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

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Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues  
Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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- 8: gb\_pr.\*
- 9: gb\_ro.\*
- 10: gb\_sts.\*
- 11: gb\_sy.\*
- 12: gb\_un.\*
- 13: gb\_vi.\*
- 14: gb\_htg.\*
- 15: gb\_pl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1721	100.0	1721	6	CQ840766 Sequence
2	1721	100.0	1721	6	CQ840768 Sequence
3	1721	100.0	1721	6	CQ840858 Sequence
4	1721	100.0	1721	6	CQ840860 Sequence
5	1721	100.0	1721	6	CQ971643 Sequence
6	1721	100.0	1721	6	CQ971645 Sequence
7	1719.4	99.9	1721	6	AR080679 Sequence
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9	1719.4	99.9	1721	6	AR125603 Sequence
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DEFINITION Sequence 9 from Patent EP1439193.  
ACCESSION CQ840766  
VERSION CQ840766.1 GI:50838370  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

Pecker, I., Vlodavsky, I. and Feinstein, E.  
Antibody directed to polypeptide having heparanase activity  
Patent: EP 1439193-A 9 21-JUL-2004;  
Insight Biopharmaceuticals Ltd. (IL); HADASIT MEDICAL RESEARCH  
SERVICES AND DEVELOPMENT LTD. (IL)  
FEATURES Location/Qualifiers

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Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1721; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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ACCESSION CQ840768  
VERSION CQ840768.1 GI:50838371  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
1  
Pecker, I., Vlodavsky, I. and Feinstein, E.  
Antibody directed to polypeptide having heparanase activity  
Patent: EP 1439193-A 11 21-JUL-2004;  
Insight Biopharmaceuticals Ltd. (IL); HADASIT MEDICAL RESEARCH  
SERVICES AND DEVELOPMENT LTD. (IL)  
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Query Match Score 1721; DB 6; Length 1721;

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VERSION	CQ840858.1 GI:50838432		
KEYWORDS	Homo sapiens (human)		
SOURCE	Homo sapiens		
ORGANISM	Homo sapiens		
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REFERENCE	1		
AUTHORS	Pecker, I., Vlodavsky, I. and Feinstein, E.		
TITLE	A nucleic acid antisense sequence to a polynucleotide encoding a polypeptide having heparanase activity		
JOURNAL	Patent: EP 1439226-A 9 21-JUL-2004; Insight Biopharmaceuticals Ltd. (IL); HADASIT MEDICAL RESEARCH SERVICES AND DEVELOPMENT LTD. (IL) Location/Qualifiers		
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## ORIGIN

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Matches 1721; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
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Qy	361	ACTTCTTAATTTTCGATCCCAAGAGGAATCAACCTTTGAAGAGAGAATTTACTGGCAAT	420						
Db	361	ACTTCTTAATTTTCGATCCCAAGAGGAATCAACCTTTGAAGAGAGAATTTACTGGCAAT	420						
Qy	421	CTCAAGTCAACAGGATATTGGCAATATATGATCCATCCCTCTGATGTGGAGAGAAGT	480						
Db	421	CTCAAGTCAACAGGATATTGGCAATATATGATCCATCCCTCTGATGTGGAGAGAAGT	480						
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Db	481	TACGGTTGGAATGGCCCTACACAGAGCAATTGCTACTCCGAGAACACTACCAAGAAAAGT	540						
Qy	541	TCAAGAACAGGACCTACTCAAGAAAGCTCTGTAGATGTGCTATACATTTTGCMAACTGCT	600						
Db	541	TCAAGAACAGGACCTACTCAAGAAAGCTCTGTAGATGTGCTATACATTTTGCMAACTGCT	600						
Qy	601	CAGGACTGGACTTGATCTTTGGCCATAATTCGTTTATTAAGAACAGCAGATTTGCAGTGA	660						
Db	601	CAGGACTGGACTTGATCTTTGGCCATAATTCGTTTATTAAGAACAGCAGATTTGCAGTGA	660						
Qy	661	ACAGTCTTAATGCTCAGTTGCTCTCGGACTACTGCTCTTCCAGGGGTATAACAATTTCTT	720						
Db	661	ACAGTCTTAATGCTCAGTTGCTCTCGGACTACTGCTCTTCCAGGGGTATAACAATTTCTT	720						
Qy	721	GGGAACTAGGCAATGAACCTAAACAGTTTCTTAAAGAGGCTGATATTTTCAATGGGT	780						
Db	721	GGGAACTAGGCAATGAACCTAAACAGTTTCTTAAAGAGGCTGATATTTTCAATGGGT	780						
Qy	781	CGCAGTTAGGAGAAGATTTTATCAATTCGATATAAATCTTAAGAAAGCTCCACCTTCAAA	840						
Db	781	CGCAGTTAGGAGAAGATTTTATCAATTCGATATAAATCTTAAGAAAGCTCCACCTTCAAA	840						
Qy	841	ATGCAAACTCTATGGTCCCTGATGTTGGTCAGCCTCGAAGAAAGACGGCTAAGATGCTGA	900						
Db	841	ATGCAAACTCTATGGTCCCTGATGTTGGTCAGCCTCGAAGAAAGACGGCTAAGATGCTGA	900						
Qy	901	AGAGCTTCTGAAGGCTGGTGGAGAAGTATGATTCAGTTTACATGGCATCATCTACTATT	960						
Db	901	AGAGCTTCTGAAGGCTGGTGGAGAAGTATGATTCAGTTTACATGGCATCATCTACTATT	960						
Qy	961	TGAATGACCGGACTGCTACCAAGGAAGATTTTCTAABACCTGATGTATGGACATTTTAA	1020						
Db	961	TGAATGACCGGACTGCTACCAAGGAAGATTTTCTAABACCTGATGTATGGACATTTTAA	1020						
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ORIGIN

Query Match		100.0%;	Score 1721;	DB 6;	Length 1721;
Best Local Similarity		100.0%;	Pred. No. 0;		
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Db	1	CTAGAGCTTTTCGACTCTCCGCTGCGCGCAGCTGCGCGGGGGAGCAGCCAGGTGAGCCCA	60		
Qy	61	AGATGCTGCTGCGCTCGAAGCCTGCGCTGCGCGCGCGCTGATGCTGCTGCTGCGGC	120		
Db	61	AGATGCTGCTGCGCTCGAAGCCTGCGCTGCGCGCGCGCTGATGCTGCTGCTGCGGC	120		
Qy	121	CGCTGGCTCCCTCTCCCTGCGCGCTGCGCGCGCTGCGCGCGCTGCGCGCGCTGCGCG	180		
Db	121	CGCTGGCTCCCTCTCCCTGCGCGCTGCGCGCGCTGCGCGCGCTGCGCGCGCTGCGCG	180		
Qy	181	ACCTGGACTTCTTCAACAGAGCGCTGCACTGCTGAGCCCTGCTGCTGCTGCTGCTCA	240		
Db	181	ACCTGGACTTCTTCAACAGAGCGCTGCACTGCTGAGCCCTGCTGCTGCTGCTGCTCA	240		
Qy	241	CCATTGACGCAACTGCGCCACGACCGCGGTTCTCATCTCTCGGTTCTCCAAAGC	300		
Db	241	CCATTGACGCAACTGCGCCACGACCGCGGTTCTCATCTCTCGGTTCTCCAAAGC	300		
Qy	301	TTCCGTACTGGCCAGAGGCTTGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	360		
Db	301	TTCCGTACTGGCCAGAGGCTTGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	360		
Qy	361	ACTTCTCTAAATTTTCGATCCCAAGAGGAATCAACTTTTGAAGAGAGGTTACTGGCAAT	420		
Db	361	ACTTCTCTAAATTTTCGATCCCAAGAGGAATCAACTTTTGAAGAGAGGTTACTGGCAAT	420		
Qy	421	CTCAAGTCAACAGGATATTTGCAAAATATGGATCCATCCCTCTCTGATGTGGAGGAGT	480		
Db	421	CTCAAGTCAACAGGATATTTGCAAAATATGGATCCATCCCTCTCTGATGTGGAGGAGT	480		
Qy	481	TACGGTTGGATGCGCTTACAGAGCAATGCTTCTCCGAGAACACTACCAGAAAAGT	540		
Db	481	TACGGTTGGATGCGCTTACAGAGCAATGCTTCTCCGAGAACACTACCAGAAAAGT	540		
Qy	541	TCAAGAACAGCACTTCTTCAAGAGCTCTGTAGATGTCTATACATTTTTCGCAACTGCT	600		
Db	541	TCAAGAACAGCACTTCTTCAAGAGCTCTGTAGATGTCTATACATTTTTCGCAACTGCT	600		
Qy	601	CAGGACTGGACTTGTATCTTTGGCCCTAAATGCGTTTATTAAGAACAGCAGATTTGAGTGA	660		
Db	601	CAGGACTGGACTTGTATCTTTGGCCCTAAATGCGTTTATTAAGAACAGCAGATTTGAGTGA	660		
Qy	661	ACAGTTCTAATGCTCAGTTGCTCTGCACTACTGCTCTTCCAGGGGTATAACATTTCTT	720		
Db	661	ACAGTTCTAATGCTCAGTTGCTCTGCACTACTGCTCTTCCAGGGGTATAACATTTCTT	720		
Qy	721	GGGAACTAGGCAATGAACCTAACAGTTTCTTAAAGAGGCTGATATTTTTCATCAATGGT	780		
Db	721	GGGAACTAGGCAATGAACCTAACAGTTTCTTAAAGAGGCTGATATTTTTCATCAATGGT	780		
Qy	781	CGCAGTTAGGAGAGATTTTATTCAATTTGCATAAACTTCTTAAGAAAGTCCACCTTCAAAA	840		

Db	781	CGCAGTTAGGAGAGATTTTATTCAATTTGCATAAACTTCTTAAGAAAGTCCACCTTCAAAA	840
Qy	841	ATCAAAACTCTATGCTCTGCTGATGTTGGTCAGCCTCGAAGAAAGAGCGCTAAGATGCTGA	900
Db	841	ATCAAAACTCTATGCTCTGCTGATGTTGGTCAGCCTCGAAGAAAGAGCGCTAAGATGCTGA	900
Qy	901	AGAGCTTCTTGAAGGCTGCTGAGAGAGTGAATGATTCAGTTACATGGCATCACTACTATT	960
Db	901	AGAGCTTCTTGAAGGCTGCTGAGAGAGTGAATGATTCAGTTACATGGCATCACTACTATT	960
Qy	961	TGAATGAGCGGACTGCTACCGAGGAGATTTTCTAAACCTCTGATGATTTGACATTTTAA	1020
Db	961	TGAATGAGCGGACTGCTACCGAGGAGATTTTCTAAACCTCTGATGATTTGACATTTTAA	1020
Qy	1021	TTTTCATCTGTGCAAAAAGTTTTCAGGTGTTGAGAGCACCAGGCTTGGCAAGAGGTCT	1080
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Qy	1081	GGTTAGGAGAAACAAAGCTCTGCATATGAGGCGGAGCGCCTTGTCTATCCGACACCTTTG	1140
Db	1081	GGTTAGGAGAAACAAAGCTCTGCATATGAGGCGGAGCGCCTTGTCTATCCGACACCTTTG	1140
Qy	1141	CAGCTGGCTTATGCTGGCTGGATAAATTTGGCCCTGTTCAGCCCGAATGGGAATAGAGTGG	1200
Db	1141	CAGCTGGCTTATGCTGGCTGGATAAATTTGGCCCTGTTCAGCCCGAATGGGAATAGAGTGG	1200
Qy	1201	TGATGAGGCAAGTATTTCTTTGGAGCAGGAACCTACCATTTAGTGGATGAAACCTTCCATC	1260
Db	1201	TGATGAGGCAAGTATTTCTTTGGAGCAGGAACCTACCATTTAGTGGATGAAACCTTCCATC	1260
Qy	1261	CTTTTACCTGATTTATGGCTATCTCTTCTGTTCAAGAAATTTGGTGGGCACCAAGGTGTTAA	1320
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Db	1381	CTGCAATCAAGGTTTAAAGAGAGGAGTAACTCTGTATGTCATAAACTTCATAACG	1440
Qy	1441	TCACCAAGTACTTTCGCGTTTACCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT	1500
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Db	1621	GTTCACCTGGGCTTCCAGGCTTCTCATATAGTTTTTTTGTGATAAGAAATGCCAAAGTTG	1680
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Qy	ACCESSION	CQ971643					
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Qy	KEYWORDS	Homo sapiens (human)					
Qy	SOURCE	Homo sapiens					
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ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Homiidae; Homo.

REFERENCE Pecker, I., Vlodavsky, I. and Feinstein, E.  
 AUTHORS Polynucleotide encoding a polypeptide having heparanase activity  
 TITLE and expression of same in transduced cells  
 JOURNAL Patent: EP 1489183-A 11 22-DEC-2004;  
 Insight Biopharmaceuticals Ltd. (IL); HADASIT MEDICAL RESEARCH  
 SERVICES And Development Ltd. (IL)

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ORIGIN  
 Query Match 100.0%; Score 1721; DB 6; Length 1721;  
 Best Local Similarity 100.0%; Pred. No. 0;  
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ACCESSION AR080679  
VERSION AR080679.1 GI:10007409  
KEYWORDS  
SOURCE Unknown.

ORGANISM Unknown.  
REFERENCE Unclassified.  
AUTHORS 1 (bases 1 to 1721)  
Pecker, I., Vlodavsky, I. and Feinstein, E.  
TITLE Polynucleotide encoding a polypeptide having heparanase activity  
and expression of same in transduced cells  
JOURNAL Patent: US 5968822-A 9 19-OCT-1999;  
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ORIGIN  
Query Match 99.9%; Score 1719.4; DB 6; Length 1721;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1720; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 1381 CTGACAACTCAAGGTATAAAGAGGAGATTTAACTCTGTATGCATAAAACCTCCATAACG 1440  
Qy 1441 TCACCAAGTACTTTCGGGTTACCTATCTCTTTTCTAACCAAGAGTGAATAAATACCTTC 1500  
Db 1441 TCACCAAGTACTTTCGGGTTACCTATCTCTTTTCTAACCAAGAGTGAATAAATACCTTC 1500  
Qy 1501 TAAGACCTTTGGGACCTCATGGATTAATTTCCAAATCTGCCAACTCAATGGTCTAACTC 1560  
Db 1501 TAAGACCTTTGGGACCTCATGGATTAATTTCCAAATCTGCCAACTCAATGGTCTAACTC 1560  
Qy 1561 TAAAGATGGTGGAGTATCAAACTTGCACCTTTTAAATGGAAAAAACCCTCTCGGCCAGGAA 1620  
Db 1561 TAAAGATGGTGGAGTATCAAACTTGCACCTTTTAAATGGAAAAAACCCTCTCGGCCAGGAA 1620  
Qy 1621 GTTCACTGGGCTTGCCAGCTTTTCTCATATAGTTTTTTTGTGATAAGAAATGCCAAAGTTG 1680  
Db 1621 GTTCACTGGGCTTGCCAGCTTTTCTCATATAGTTTTTTTGTGATAAGAAATGCCAAAGTTG 1680  
Qy 1681 CTGCTTGCACTCGAAAAATAAATAATATAGTCTCTGACACTG 1721

Db	1681	CTGCTTGCATCTGAAATAAATAATACTAGTCTGCACACTG	1721	linear	PAT 31-AUG-2000	Qy	661	ACAGTTCTAATGCTCAGTTGCTCCTCGACATCTGCTCTTCCAAAGGGGTATAACAATTTCTT	720
						Db	661	ACAGTTCTAATGCTCAGTTGCTCCTCGACATCTGCTCTTCCAAAGGGGTATAACAATTTCTT	720
RESULT 8	AR080680	AR080680	1721 bp	DNA		Qy	721	GGGAATAGCAATGAACCTTAACAGATTTCTTAAAGAGCTGATATTTTTCATCAATGGGT	780
LOCUS	Sequence 11 from patent US 5968822.					Db	721	GGGAATAGCAATGAACCTTAACAGATTTCTTAAAGAGCTGATATTTTTCATCAATGGGT	780
DEFINITION	AR080680					Qy	781	CGCAGTTAGGAGAGATTTTATTAATGTCATAAACTTCTTAAGAAAAGTCACCTTCAAAA	840
ACCESSION	AR080680					Db	781	CGCAGTTAGGAGAGATTTATTAATGTCATAAACTTCTTAAGAAAAGTCACCTTCAAAA	840
VERSION	AR080680.1	GI:10007410				Qy	841	ATGCAAAAATCTATGCTCTGATGTTGGTTCAGCTCGAGAGAGAGCGCTTAAGATGCTGA	900
KEYWORDS	Unknown.					Db	841	ATGCAAAAATCTATGCTCTGATGTTGGTTCAGCTCGAGAGAGAGCGCTTAAGATGCTGA	900
SOURCE	Unknown.					Qy	901	AGAGCTTCTGAGAGCTGTTGAGAGAGATTTGATTCAGTTACATGSCATCCTACTATT	960
ORGANISM	Unclassified.					Db	901	AGAGCTTCTGAGAGCTGTTGAGAGAGATTTGATTCAGTTACATGSCATCCTACTATT	960
REFERENCE	1 (bases 1 to 1721)					Qy	961	TGAATGGAACGAGCTGCTACCCAGGGAAGATTTTCTAAACCTCTGATGTATTGGAATTTT	1020
AUTHORS	Pecker, I., Vlodavsky, I. and Feinstein, E.					Db	961	TGAATGGAACGAGCTGCTACCCAGGGAAGATTTTCTAAACCTCTGATGTATTGGAATTTT	1020
TITLE	Polynucleotide encoding a polypeptide having heparanase activity					Qy	1021	TTTTCATCTGTGCAAAAAGTTTTCACAGTGGTTCAGAGCACCAGGCTGGCAAGAGTCT	1080
JOURNAL	Patent: US 5968822-A 11 19-OCT-1999;					Db	1021	TTTTCATCTGTGCAAAAAGTTTTCACAGTGGTTCAGAGCACCAGGCTGGCAAGAGTCT	1080
FEATURES	Location/Qualifiers					Qy	1081	GGTTAGAGAAAACAAGCTCTGCATATGAGAGCGGAGGCGCTTGTCTATCCGACACCTT	1140
source	1. .1721					Db	1081	GGTTAGAGAAAACAAGCTCTGCATATGAGAGCGGAGGCGCTTGTCTATCCGACACCTT	1140
ORIGIN	/organism="unknown"					Qy	1141	CAGCTGGCTTTATGCTGGGATAAATTTGGGCTGTGAGCGGAGGCGCTTGTCTATCCGACACCTT	1200
	/mol_type="unassigned DNA"					Db	1141	CAGCTGGCTTTATGCTGGGATAAATTTGGGCTGTGAGCGGAGGCGCTTGTCTATCCGACACCTT	1200
	Query Match 99.9%; Score 1719.4; DB 6; Length 1721;					Qy	1201	TGATGAGGCAAGTATTTCTTGGAGCAGGAAATACCATTTAGTGGATGAAAACCTTCGATC	1260
	Best Local Similarity 99.9%; Pred. No. 0;					Db	1201	TGATGAGGCAAGTATTTCTTGGAGCAGGAAATACCATTTAGTGGATGAAAACCTTCGATC	1260
	Matches 1720; Conservative 0; Mismatches 1; Indels 0; Gaps 0;					Qy	1261	CTTTTACCTGATTTATGGCTATCTCTTCTGTTCAAGAAATTTGGTGGGACCAAGGTGTAA	1320
						Db	1261	CTTTTACCTGATTTATGGCTATCTCTTCTGTTCAAGAAATTTGGTGGGACCAAGGTGTAA	1320
1	CTAGAGCTTTGCACTCTCCGCTGGCGAGCTGCGCGAGCTGGCGGGGGAGAGACCCAGGTGAGCCCA	60				Qy	1321	TGCAAGAGCTGCAAGGTTTCAAGAGAGAGAGCTTCGAGTATACCTTTTTCATTGTCACAAACA	1380
1	CTAGAGCTTTGCACTCTCCGCTGGCGAGCTGCGCGAGCTGGCGGGGGAGAGACCCAGGTGAGCCCA	60				Db	1321	TGCAAGAGCTGCAAGGTTTCAAGAGAGAGAGCTTCGAGTATACCTTTTTCATTGTCACAAACA	1380
61	AGATGCTGCTGCGTCCGAAGCTGCGCTGCGCGAGCTGGCGCGCTGCTGCTCTCTGGGGC	120				Qy	1381	CTGACCAATCCAGGTATTAAGAGAGAGATTTTAACTCTGTATGCCATAAAACCTCCATAACG	1440
61	AGATGCTGCTGCGTCCGAAGCTGCGCTGCGCGAGCTGGCGCGCTGCTGCTCTCTGGGGC	120				Db	1381	CTGACCAATCCAGGTATTAAGAGAGAGATTTTAACTCTGTATGCCATAAAACCTCCATAACG	1440
121	CGCTGGGTCCCTCTCCCTCTGGCGCTGCGCGAGCTGGCGCGAGCAGCAGGAGCTCGTGG	180				Qy	1441	TCACCAAGTACTTGGCGGTACCCCTATCCTTTTCTAACCAAGCAAGTGGATTAACCTTC	1500
121	CGCTGGGTCCCTCTCCCTCTGGCGCTGCGCGAGCTGGCGCGAGCAGCAGGAGCTCGTGG	180				Db	1441	TCACCAAGTACTTGGCGGTACCCCTATCCTTTTCTAACCAAGCAAGTGGATTAACCTTC	1500
181	ACCTGAGCTTTTCAACCCAGAGCGCTGCACTGGTGGAGCCCTCTCTGCTGCTGCTGCA	240				Qy	1501	TABAGCTTTGGGACCTCATGGATTTCTCCAAATCTGTCCAACTCAATGGTCTTAACTC	1560
181	ACCTGAGCTTTTCAACCCAGAGCGCTGCACTGGTGGAGCCCTCTCTGCTGCTGCTGCA	240				Db	1501	TABAGCTTTGGGACCTCATGGATTTCTCCAAATCTGTCCAACTCAATGGTCTTAACTC	1560
241	CCATTGACGCCAACCTGGCCACGAGCCCGGGTTCTCTCATCTCTGGGTCTCCAAAGC	300				Qy	1561	TAAAGATGGTGGATGATCAAAACCTTGCCACTTTTAAATGGAACAACTCTCCGGCCAGAA	1620
241	CCATTGACGCCAACCTGGCCACGAGCCCGGGTTCTCTCATCTCTGGGTCTCCAAAGC	300				Db	1561	TAAAGATGGTGGATGATCAAAACCTTGCCACTTTTAAATGGAACAACTCTCCGGCCAGAA	1620
301	TTGCTACTTTGGCCAGAGGCTTGTCTCTGCTACCTGAGGTTTGGTGGCACCAGACAG	360				Qy	1621	GTTTCACTGGGCTTGGCAGCTTTCTCATATAGTTTTTTTTTGTGATAAGAAATGCCAAAGTTG	1680
301	TTGCTACTTTGGCCAGAGGCTTGTCTCTGCTACCTGAGGTTTGGTGGCACCAGACAG	360				Db	1621	GTTTCACTGGGCTTGGCAGCTTTCTCATATAGTTTTTTTTTGTGATAAGAAATGCCAAAGTTG	1680
361	ACTTCTTAAATTTTCATCCCAAGAGGAATCAACCTTTTGAAGAGAGATTAAGTGGCAAT	420				Qy	1681	CTGCTTGCATCTGAAATATAATAATACTAGTCTGCACACTG	1721
361	ACTTCTTAAATTTTCATCCCAAGAGGAATCAACCTTTTGAAGAGAGATTAAGTGGCAAT	420				Db	1681	CTGCTTGCATCTGAAATATAATAATACTAGTCTGCACACTG	1721
421	CTCAAGTCAACAGGATATTTGCAATATGATTCATCCCTCTCTGATGTGGAGAGAGT	480							
421	CTCAAGTCAACAGGATATTTGCAATATGATTCATCCCTCTCTGATGTGGAGAGAGT	480							
481	TACGGTTGGAATGGCCCTACAGAGCAATTTGCTTACTCCGAGAACACTACACAGAAAAGT	540							
481	TACGGTTGGAATGGCCCTACAGAGCAATTTGCTTACTCCGAGAACACTACACAGAAAAGT	540							
541	TCAGAAACAGCACCTACTCAAGAGCTCTGTAGATGTCTATACACTTTTTCGAAACTGCT	600							
541	TCAGAAACAGCACCTACTCAAGAGCTCTGTAGATGTCTATACACTTTTTCGAAACTGCT	600							
601	CAGGACTGGACTTGTATCTTTGGCCCTAAATGCGTTATTAAGAACAGCAGATTTGCAAGTGA	660							
601	CAGGACTGGACTTGTATCTTTGGCCCTAAATGCGTTATTAAGAACAGCAGATTTGCAAGTGA	660							



RESULT 9	AR125603	1721 bp	DNA	linear	PAT 16-MAY-2001
LOCUS	Sequence 1 from patent US 6177545.				
DEFINITION	AR125603				
ACCESSION	AR125603				
VERSION	AR125603.1	GI:14111665			
KEYWORDS	Unknown.				
SOURCE	Unknown.				
ORGANISM	Unclassified.				
REFERENCE	1 (bases 1 to 1721)				
AUTHORS	Pecker, I., Vlodavsky, I., Friedman, Y. and Perets, T.				
TITLE	Heparanase specific molecular probes and their use in research and medical applications				
JOURNAL	Patent: US 6177545-A 1 23-JAN-2001;				
FEATURES	Location/Qualifiers				
source	1..1721				
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	/mol_type="unassigned DNA"				
ORIGIN					
Query Match	99.9%;	Score 1719.4;	DB 6;	Length 1721;	
Best Local Similarity	99.9%;	Pred. No. 0;			
Matches 1720;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;	
Qy	1	CTAGAGCTTTCCGACTCTCCGCTGCGCGCAGCTGCGCGGGGAGCAGCCAGGTGAGCCCA	60		
Db	1	CTAGAGCTTTCCGACTCTCCGCTGCGCGCAGCTGCGCGGGGAGCAGCCAGGTGAGCCCA	60		
Qy	61	AGATGCTGCTCGCTCGAAGCTCGCTGCGCGCGCGCTGATCTGCTGCTCTGGGGC	120		
Db	61	AGATGCTGCTCGCTCGAAGCTCGCTGCGCGCGCGCTGATCTGCTGCTCTGGGGC	120		
Qy	121	CGCTGGGTCCCTCTCCCTGGCGCCTGCGCCGACCTGCGCAAGCAAGACGCTCGTGG	180		
Db	121	CGCTGGGTCCCTCTCCCTGGCGCCTGCGCCGACCTGCGCAAGCAAGACGCTCGTGG	180		
Qy	181	ACCTGGACTTCTTCCACCAGAGCGCTGCGACCTGCTGAGCGCCCTGCTGTCGCTCA	240		
Db	181	ACCTGGACTTCTTACCAGAGCGCTGCGACCTGCTGAGCGCCCTGCTGTCGCTCA	240		
Qy	241	CCATTGACGCCAACTGGCCACGACCGCGGTTCTCTCATCTCTGGTTCTCCAAAGC	300		
Db	241	CCATTGACGCCAACTGGCCACGACCGCGGTTCTCTCATCTCTGGTTCTCCAAAGC	300		
Qy	301	TTCTGACTTGGCCAGAGGCTTGTCTCTGCTGCTACCTGAGTTTGGTGGCAACAGACAG	360		
Db	301	TTCTGACTTGGCCAGAGGCTTGTCTCTGCTGCTACCTGAGTTTGGTGGCAACAGACAG	360		
Qy	361	ACTTCCCTAAATTTTCGATCCCAAGAGGAATCAACCTTTGAGAGAGAGTTTACTGGCAAT	420		
Db	361	ACTTCCCTAAATTTTCGATCCCAAGAGGAATCAACCTTTGAGAGAGAGTTTACTGGCAAT	420		
Qy	421	CTCAAGTCAACAGGATATTTGCAATATGATCCATCCCTCTCTGATGTGGAGAGAGT	480		
Db	421	CTCAAGTCAACAGGATATTTGCAATATGATCCATCCCTCTCTGATGTGGAGAGAGT	480		
Qy	481	TACGGTTGGAATGCCCCTACAGAGCAATTTGCTACTCCGAGAACATCTACAGAAAAAGT	540		
Db	481	TACGGTTGGAATGCCCCTACAGAGCAATTTGCTACTCCGAGAACATCTACAGAAAAAGT	540		
Qy	541	TCAAGAACAGCACTACTCAAGAGCTCTGTAGATGTCTATACACTTTTGCAAACTGCT	600		
Db	541	TCAAGAACAGCACTACTCAAGAGCTCTGTAGATGTCTATACACTTTTGCAAACTGCT	600		
Qy	601	CAGACTGGACTTGTATCTTTGGCCTAAATGGTTATTAAAGAACAGAGATTGCAAGTGA	660		
Db	601	CAGACTGGACTTGTATCTTTGGCCTAAATGGTTATTAAAGAACAGAGATTGCAAGTGA	660		
Qy	661	ACAGTTCTAATGCTCAGTTGCTCTCGACTACTGCTCTTCCAGGGGTATAACATTTCTT	720		
Db	661	ACAGTTCTAATGCTCAGTTGCTCTCGACTACTGCTCTTCCAGGGGTATAACATTTCTT	720		

RESULT 10  
AR125604  
LOCUS

Sequence 3 from patent US 6177545.  
DEFINITION

AR125604 1721 bp DNA linear PAT 16-MAY-2001



ACCESSION ARI25604  
 VERSION ARI25604.1 GI:14111666  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 REFERENCE 1 (bases 1 to 1721)  
 Pecker, I., Vlodavsky, I., Friedman, Y. and Perets, T.  
 TITLE Heparanase specific molecular probes and their use in research and medical applications  
 JOURNAL Patent: US 6177545-A 3 23-JAN-2001;  
 FEATURES  
 source Location/Qualifiers  
 1..1721  
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ORIGIN

Query Match 99.9%; Score 1719.4; DB 6; Length 1721;  
 Best Local Similarity 99.9%; Pred. No. 0;  
 Matches 1720; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CTAGAGCTTTTCAGACTCTCCGCTGCGCGCAGCTGGCGGGGGAGCAGCCAGGTGAGCCCA 60  
 Db 1 CTAGAGCTTTTCAGACTCTCCGCTGCGCGCAGCTGGCGGGGGAGCAGCCAGGTGAGCCCA 60

Qy 61 AGATGCTGCTCGAGCTCGAAGCTGCGCTGCGCGCGCGCTGATGCTGCTGCTGCTGCGGC 120  
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Qy 121 CGCTGGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180  
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Qy 181 ACCTGGAGCTTTTCAACCCAGAGCGCTGCGACCTGGTGGAGCCCTGCTGCTGCTGCTGCTGCT 240  
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Qy 241 CCATTGAGCCCAACCTGCGCCAGGACCGCGGTTCTCATCTCTGCTGCTGCTGCTGCTGCTGCT 300  
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Qy 301 TTGCTACTTGGCCAGAGCTTGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360  
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Qy 361 ACTTCTTAATTTTCGATCCCAAGAGGAATCAACCTTTTGAAGAGAGAGTACTTGCGCAAT 420  
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Qy 421 CTCAGTCAACCCAGGATTTTGCAGATATGATGATCCATCCCTCTGATGCTGGAGGAGAGT 480  
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Qy 481 TAGCGTTGGAATGCGCCCTACAGAGCAATGCTACTCCGAGAACACTACAGAAAAGT 540  
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Qy 541 TCAAGACAGACCTACTCAAGAGCTCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCT 600  
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Qy 601 CAGGACTGGACTTGTATCTTTGGCCCTAAATGGCTTATTAAGAACAGCAGAGATTTGCGAGTGA 660  
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Qy 661 ACAGTCTTAATGCTCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720  
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Qy 721 GGGNACTAGGCAATGAACCTTAACAGTTTCCCTTAAGAGGCTGATATTTTTCATCAATGGGT 780  
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## RESULT 11

BD074427

LOCUS

DEFINITION

expression of the polypeptide in induced cell.

ACCESSION

BD074427

VERSION

BD074427.1

KEYWORDS

JP 2001514855-A/8.

BD074427 1721 bp DNA linear PAT 27-AUG-2002  
 Polynucleotide encoding polypeptide having heparanase activity and  
 expression of the polypeptide in induced cell.  
 BD074427  
 BD074427.1 GI:22620030  
 JP 2001514855-A/8.

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 Db 1681 CTGCTTGCATCTGAAATATAATATATAGTCTCTGACACTG 1721

SOURCE unidentified  
ORGANISM unclassified  
REFERENCE 1 (bases 1 to 1721)  
AUTHORS Pecker,I., Vlodavsky,I. and Elena,F.  
TITLE Polynucleotide encoding polypeptide having heparanase activity and expression of the polypeptide in induced cell  
JOURNAL Patent: JP 2001514855-A 8 18-SEP-2001;  
INSIGHT STRATEGY & MARKETING LTD, HADASIT MEDICAL RESEARCH SERVICES & DEVELOPMENT LTD  
COMMENT OS Nucleic acid  
PN JP 2001514855-A/8  
PD 18-SEP-2001  
PF 31-AUG-1998 JP 2000508806  
PR 02-SEP-1997 US 08/922170,02-JUL-1998 US 09/109386 PI  
IRIS PECKER,ISRAEL VLODAVSKY,FEINSTEIN ELENA  
PC C12N15/09,A61K38/00,A61P9/10,A61P17/00,A61P29/00,A61P35/00,PC A61P37/00,  
PC A61P43/00,C12N5/10,C12N9/24,C12Q1/68,G01N33/15,G01N33/50// PC A61K39/395  
PC A61K39/395,C12N15/00,A61K37/02,C12N5/00  
CC Polynucleotide encoding polypeptide having  
heparanase activity  
and  
CC expression of the polypeptide in induced cell FH Key  
Location/Qualifiers  
FT source 1..1721 /organism='Nucleic acid'.  
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Query Match 99.9%; Score 1719.4; DB 6; Length 1721;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1720; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CTAGAGCTTTCGACTCCCGTGTGCGCGAGCTGGCGGGGGAGCAGCCAGGTGAGCCCA 60  
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Qy 61 AGATGCTGCTCGCTCGAAGCTCGGCTGCGCGCGCGCTGATGCTGCTGCTCTGGGC 120  
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Qy 121 CGCTGGGTCCCTCTCCCTGCGCGCTGCGCGCGCGCTGATGCTGCTGCTCTGGGC 180  
Db 121 CGCTGGGTCCCTCTCCCTGCGCGCTGCGCGCGCGCTGATGCTGCTGCTCTGGGC 180

Qy 181 ACCTGGACTTCTTCAACCCAGGAGCGGTGCACTGGTGAAGCCCTCGTTCCTGCTCA 240  
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RESULT 12  
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LOCUS BD074428 1721 bp DNA linear PAT 27-AUG-2002  
DEFINITION Polynucleotide encoding polypeptide having heparanase activity and expression of the polypeptide in induced cell.  
ACCESSION BD074428  
VERSION BD074428.1 GI:22620031  
KEYWORDS JP 2001514855-A/9.  
SOURCE unidentified  
ORGANISM unclassified.  
REFERENCE 1 (bases 1 to 1721)  
AUTHORS Pecker, I., Vlodaysky, I. and Elena, F.  
TITLE Polynucleotide encoding polypeptide having heparanase activity and expression of the polypeptide in induced cell  
JOURNAL Patent: JP 2001514855-A 9 18-SEP-2001;  
INSIGHT STRATEGY & MARKETING LTD, HADASIT MEDICAL RESEARCH SERVICES & DEVELOPMENT LTD  
COMMENT OS Nucleic acid  
PN JP 2001514855-A/9  
PD 18-SEP-2001  
PF 31-AUG-1998 JP 200050806  
PR 02-SEP-1997 US 08/922170, 02-JUL-1998 US 09/109386 P1  
IRIS PECKER, ISRAEL VLODASKY, FEINSTEIN ELENA  
PC C12N15/09, A61K38/00, A61P9/10, A61P17/00, A61P29/00, A61P35/00, PC A61P37/00,  
PC A61P43/00, C12N5/10, C12N9/24, C12Q1/68, G01N33/15, G01N33/50// PC A61K39/395,  
PC A61K39/395, C12N15/00, A61K37/02, C12N5/00  
CC Polynucleotide encoding polypeptide having heparanase activity  
CC and  
CC expression of the polypeptide in induced cell FH Key  
FT Location/Qualifiers (63)..(1691).  
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ORIGIN

Query Match 99.98; Score 1719.4; DB 6; Length 1721;  
Best Local Similarity 99.98; Pred. No. 0;  
Matches 1720; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy 61 AGATGCTGCTCGGCTCGAAGCCTGCGCTGCCGCGCGCTGATGCTGCTCTCTGGGC 120  
Db 61 AGATGCTGCTCGGCTCGAAGCCTGCGCTGCCGCGCGCTGATGCTGCTCTCTGGGC 120

Qy 121 CGCTGGGTCCGCTCTCCCTGGGCGCTGCGCGACCTGCGCAGCAGCAGAGCTGCTGG 180  
Db 121 CGCTGGGTCCGCTCTCCCTGGGCGCTGCGCGACCTGCGCAGCAGCAGAGCTGCTGG 180

Qy 181 ACCTGGACTTCTTCAACCAGGAGCGCTGCACCTGGTGGCCCTCGTCTCTGTCGCTCA 240  
Db 181 ACCTGGACTTCTTCAACCAGGAGCGCTGCACCTGGTGGCCCTCGTCTCTGTCGCTCA 240

Qy 241 CCATTGACGCCAACTGGGCCACGAGCCCGGGTTCTCTCATCTCTCTGGGTTCTCCAAAGC 300

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Db	1381	CTGACAACTCCAAAGGTATAAAGAGAGATTTAACTCTGTATGCCATAAAACCTCATTAACG	1440
Qy	1441	TCACCAAGTACTTGGGGTACCCTTATCCCTTTCTTAACAAGCAAGTGGATAAAATACCTTC	1500
Db	1441	TCACCAAGTACTTGGGGTACCCTTATCCCTTTCTTAACAAGCAAGTGGATAAAATACCTTC	1500
Qy	1501	TAAGACCTTTGGGACCTCATGGATTAATCTTCCAACTCTGTAAGAAATGCCAAAGTTG	1560
Db	1501	TAAGACCTTTGGGACCTCATGGATTAATCTTCCAACTCTGTAAGAAATGCCAAAGTTG	1560
Qy	1561	TAAAGATGGTGGATGATCAAAACCTTGGCACCTTTAAATGGAAAAACCTTCGGGCCAGGAA	1620
Db	1561	TAAAGATGGTGGATGATCAAAACCTTGGCACCTTTAAATGGAAAAACCTTCGGGCCAGGAA	1620
Qy	1621	GTTCACTGGGCTTGCCAGCTTTCTCATATAGTTTTTTTGTGATAAGAAATGCCAAAGTTG	1680
Db	1621	GTTCACTGGGCTTGCCAGCTTTCTCATATAGTTTTTTTGTGATAAGAAATGCCAAAGTTG	1680
Qy	1681	CTGCTTGATCTGAAAATAAAATATATAGTCTGACACTG	1721
Db	1681	CTGCTTGATCTGAAAATAAAATATATAGTCTGACACTG	1721
RESULT 13			
BD193236		1721 bp	DNA linear
LOCUS			PAT 17-JUL-2003
DEFINITION	BD193236	Heparanase specific molecular probes and their use in research and medical applications.	
ACCESSION	BD193236		
VERSION	BD193236.1	GI:33002975	
KEYWORDS	JP 2002512533-A/1.		
SOURCE	Streptococcus equi		
ORGANISM	Streptococcus equi		
REFERENCE	Bacteria: Firmicutes; Lactobacilliales; Streptococcaceae; Streptococcus.		
AUTHORS	1 (bases 1 to 1721)		
TITLE	Pecker, I., Vlodavsky, I., Friedman, Y. and Perets, T.		
JOURNAL	Heparanase specific molecular probes and their use in research and medical applications		
COMMENT	Patent: JP 2002512533-A 1 23-APR-2002; INSIGHT STRATEGY & MARKETING LTD, HADASIT MEDICAL RESEARCH SERVICES & DEVELOPMENT LTD		
PN	JP 2002512533-A/1		
PD	23-APR-2002		
PF	29-APR-1999	JP 1999555528	
PI	01-MAY-1998	US 09/071739	
PR	IRIS PECKER, ISRAEL VLODAVSKY, Yael FRIEDMAN, TUVIA PERETS		
PC	C07K16/00, C07K16/40, G01N33/53, C07H21/02, C7H21/04, A61K39/395		
CC	nucleic acid		
FEAT Key	Location/Qualifiers.		
source	1. 1721		
ORIGIN	/organism="Streptococcus equi"		
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Query Match	99.9%	Score 1719.4;	DB 6; Length 1721;
Best Local Similarity	99.9%	Pred. No. 0;	
Matches 1720;	Conservative 0;	Mismatches 1;	Indels 0; Gaps 0;
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Qy	61	AGATGCTGCTGGCTCGAAGCTTGGCTGGCGCGCGCTGATGCTGCTCTCTGGGGC	120
Db	61	AGATGCTGCTGGCTCGAAGCTTGGCTGGCGCGCGCTGATGCTGCTCTCTGGGGC	120

Qy	121	CGCTGGTCCCTCTCCCTGGCGCCCTGCTCCCGAAGCTGCGCAAGCACAGAGCGTCTCGTG	180
Db	121	CGCTGGTCCCTCTCCCTGGCGCCCTGCTCCCGAAGCTGCGCAAGCACAGAGCGTCTCGTG	180
Qy	181	ACCTGGAATTTTCAACCCAGAGCCGCTGCACTGCTGAGCCCTCGTTCCTGTCGCTCA	240
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Qy	241	CAATTGAGCGCAACCTTGGCCACCGGACCGCGGTTCTCATCTCTCTGGGTTCTCCAAAGC	300
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Qy	841	ATGCAAACTCTATGGTCTCTGATGTTGGTCAAGAACAGCGCTTAAGATGCTGA	900
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Qy	901	AGAGCTTCTGAAAGGCTGGTGGAGAGTGAATGATTCAGTTACATGGCATCACTACTATT	960
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Qy	1081	GGTTAGGAGAAAACAGCTCTGCATATGAGGCGGAGCGCTTGTCTATCCGACACCTTTG	1140
Db	1081	GGTTAGGAGAAAACAGCTCTGCATATGAGGCGGAGCGCTTGTCTATCCGACACCTTTG	1140
Qy	1141	CAGCTGCTTTTATGTGCTGATTAATTTGGGCTGTGAGCGCCGAGTGAAGTGG	1200
Db	1141	CAGCTGCTTTTATGTGCTGATTAATTTGGGCTGTGAGCGCCGAGTGAAGTGG	1200
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RESULT 14  
BD193237  
LOCUS BD193237 1721 bp DNA linear PAT 17-JUL-2003  
DEFINITION Heparanase specific molecular probes and their use in research and medical applications.  
ACCESSION BD193237  
VERSION BD193237.1 GI:33002976  
KEYWORDS JP 2002512533-A/2.  
SOURCE Streptococcus equi  
ORGANISM Streptococcus equi  
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Streptococcus.  
REFERENCE 1 (bases 1 to 1721)  
AUTHORS Pecker, I., Vlodavsky, I., Friedman, Y. and Perets, T.  
TITLE Heparanase specific molecular probes and their use in research and medical applications  
JOURNAL Patent: JP 2002512533-A 2 23-APR-2002;  
INSIGHT STRATEGY & MARKETING LTD, HADASIT MEDICAL RESEARCH SERVICES & DEVELOPMENT LTD  
COMMENT PN JP 2002512533-A/2  
PD 23-APR-2002  
PF 29-APR-1999 JP 1999555528  
PR 01-MAY-1998 US 09/071739  
PI IRIS PECKER, ISRAEL VLODAVSKY, Yael FRIEDMAN, TUVIA PERETS PC  
C07K16/00, C07K16/40, G01N33/53, C07H21/02, C7H21/04, A61K39/395 CC  
nucleic acid  
FH Key Location/Qualifiers  
FT CDS Location/Qualifiers  
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## ORIGIN

Query Match 99.9%; Score 1719.4; DB 6; Length 1721;  
Best Local Similarity 99.9%; Pred. No. 0;

Matches 1720; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
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RESULT 15

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LOCUS 1721 bp DNA linear PAT 17-JUL-2003  
DEFINITION Cells genetically modified for expressing recombinant heparanase  
and method, and method of purifying recombinant heparanase.  
ACCESSION BD205238  
VERSION BD205238.1 GI:33015008  
KEYWORDS JP 2002513560-A/1.  
SOURCE unidentified  
ORGANISM unclassified.  
REFERENCE 1 (bases 1 to 1721)  
AUTHORS Artzi,H.B., Herzhkovitz,M.A., Zeevi,O.Y., Pecker,I., Peleg,Y.,  
Shlomi,Y., Moskowitiz,H., Miron,D., Gilboa,A. and Mimon,M.  
TITLE Cells genetically modified for expressing recombinant heparanase  
and method, and method of purifying recombinant heparanase  
JOURNAL Patent: JP 2002513560-A 1 14-MAY-2002;  
COMMENT INSIGHT STRATEGY AND MARKETING LTD  
OS Unidentified  
PN JP 2002513560-A/1  
PD 14-MAY-2002  
PF 29-APR-1999 JP 2000547200  
PR 01-MAY-1998 US 09/071618,02-MAR-1999 US 09/260038 PI  
HANNA BEN ARTZI,MATY AYAL HERSHKOVITZ,ORON YACOBY ZEEVI,IRIS PI  
PECKER,  
PI YOAV PELEG,YINON SHLOMI,HAIM MOSKOWITZ,DEPHNA MIRON,AYELET PI  
GILBOA,

PI MADELENE MIMON  
PC C12N15/09, C07K16/40, C12N1/19, C12N1/21, C12N5/10, C12N9/24, C12N15/ PC  
00, C12N5/00  
CC Strandedness: Double;  
CC Topology: Linear;  
CC Cells genetically modified for expressing recombinant CC  
heparanase and  
CC method, and method of purifying recombinant heparanase. FH  
Key source Location/Qualifiers  
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/db\_xref='taxon:32644'  
ORIGIN  
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Best Local Similarity 99.9%; Pred. No. 0;  
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Db 61 AGATGCTGTGCGCTGGAAGCTTGGCTGCGCGCGCGCTGATGCTGCTCTCTCTGGGGC 120  
Qy 121 CGCTGGGTCCCTCTCCCTGCGCGCGCTGCGCGCGCGCTGCGCGCGCGCTGATGCTGCTGG 180  
Db 121 CGCTGGGTCCCTCTCCCTGCGCGCGCTGCGCGCGCGCTGCGCGCGCGCTGATGCTGCTGG 180  
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Qy 1441 TCACCAAGTACTTGGGTTACCCCTATCTCTTTTCTAACAAGCAAGTGGATAAATACCTTC 1500  
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GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.  
OM protein - protein search, using sw model  
Run on: February 27, 2006, 17:47:12 ; Search time 42 Seconds  
(without alignments)  
1243.945 Million cell updates/sec  
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Perfect score: 2841  
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Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5  
Searched: 283416 seqs, 96216763 residues  
Total number of hits satisfying chosen parameters: 283416  
Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries  
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1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	893.5	31.5	480	2	J47506
2	417	14.7	521	2	T45608
3	169.5	6.0	190	2	T01953
4	112	3.9	2298	2	T49648
5	111	3.9	670	2	T10666
6	111	3.9	688	2	S32961
7	110.5	3.9	356	2	F64383
8	107.5	3.8	575	2	T12094
9	106	3.7	670	2	T38446
10	105.5	3.7	411	2	S74760
11	105.5	3.7	879	2	E91031
12	104.5	3.7	788	1	S00652
13	104	3.7	432	2	F70411
14	104	3.7	796	2	D97065
15	104	3.7	2013	2	A11489
16	103.5	3.6	500	2	D87541
17	103.5	3.6	676	2	AF1153
18	102	3.6	879	2	F85875
19	102	3.6	897	2	G02529
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21	101.5	3.6	746	2	T46821
22	101.5	3.6	746	2	A95420
23	101	3.6	594	2	A82913
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34	98.5	3.5	804	2	G71546
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36	98	3.4	644	2	A97268
37	98	3.4	716	1	C60008
38	97.5	3.4	511	2	S61166
39	97	3.4	379	2	A69974
40	97	3.4	437	1	A48061
41	97	3.4	726	2	C86085
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43	97	3.4	760	2	T34414
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45	96.5	3.4	621	2	A95250

NADH2 dehydrogenas  
beta-fructofuranos  
toxin secretion AB  
hypothetical prote  
probable DNA gyras  
hypothetical prote  
methionyl-tRNA syn  
RNA-directed RNA p  
cystathionine gamm  
translation releas  
catalase, hydroper  
hydroperoxidase HP  
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conserved hypotet  
choline binding pr

ALIGNMENTS

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heparanase protein 2a - human  
C:Species: Homo sapiens (man)  
C:Date: 17-Nov-2000 #sequence\_revision 17-Nov-2000 #text\_change 09-Jul-2004  
C:Accession: JC7506  
R:McKenzie, E.; Tyson, K.; Stamps, A.; Smith, P.; Turner, P.; Barry, R.; Hircock, M.; F  
Biochem. Biophys. Res. Commun. 276, 1170-1177, 2000  
A:Title: Cloning and expression profiling of Hpa2, a novel mammalian heparanase family  
A:Reference number: JC7506  
A:Accession: JC7506  
A:Molecule type: mRNA  
A:Residues: 1-480 <MCK>  
A:Cross-references: UNIPROT:Q9HB39, UNIPARC:UPI000003888A, GB:AF282885  
C:Comment: This protein, an intracellular membrane-bound enzyme, has biological and ther  
therapies.  
C:Genetics:  
A:Gene: hpa2a  
A:Map position: 10q23-10q24  
C:Keywords: heparin binding; membrane bound

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Qy	20	PLGLSPGAL	-----PRPA-----	QAQVVVDLFFQEPHLVSPS	55	
Db	18	PPACLAPGALYLALLHLHLSLSSQAGDRRPLPVDRAAGLKEKTLILLDVSTKNPVRTVNE	77			
Qy	56	FLSVTIDANLATDPRFLLILGSPKRLTARGLSPAVLRFGTGTDFLIF---	DPKKEST	111		
Db	78	FLSLQDPSIIHD-GWLDLFLSSKRLVTLAGLSPAFLRFGGKRTDFLQFNLRNPAKSR-	135			
Qy	112	FEERSYQSQVNQDICKYGISPPDVEEKLREWPYQELLRREHYQKFKFNSTYSRSSVD	171			
Db	136	-----GGGPD-----	YLLKNYE-----	148		
Qy	172	VLYTFANCGLDLIFGLNALLRTADLQWSSNAQLLLDYCSSKGYNISWELGNPNPSFLK	231			
Db	149	-----DEPNYRT	156			
Qy	232	KADIFINGSOLGEDFTQLHKLK-LSTFKNAKLYGPDVGOPRRTAKMLKSLFKAGEVI	290			
Db	157	MHGRAVNSQLGKDYQLKSLQLPIRIYGRASLYGNIGRPRKRVKNTALLDGFMKVAGSTV	216			
Qy	291	DSVTWHYHLYNGRTATREFLPNDVLDFITSSQKVQFVVESTRPGKVKWLGETSSAYGG	350			
Db	217	DATWQHCHIDGRVVKVMDFLKTRLDLTDSDQIRKQKVNTYTPGKKIWLGVVTSAG	276			
Qy	351	GAPLLSDTFAAGPMWLDKLGSLARMGIEVVMQVFFGAGNYHLVDENFDPLPDYWLSLFL	410			
Db	277	GTNNLSDSVAAGFLWLTLMGLANQGDVIRHSFFDHGYNHLVDQNFNPLPDYWLSLLY	336			

Qy 411 KKLVTGTVLMASVOGSKRR-----KLVYLHCTNTDNPYKEGDLTLIYAINLHNTV 461  
Db 337 KRLTIGPKVLAVHVAAGLQKRPGRVIRDKLRIYAHCTNNHNNYVRSITLFIINLHRSR 396  
Qy 462 KYLRPLYPFNSKNQVDKYLRLPLGPHGLLSKSVQLNGLTKMVDQDTLPPLMEKPLRPGSS 521  
Db 397 KKIKLAGTLRDKLVHQLYLPQYGOGLKSKSVQLNGQLVNVDDGTLPELKPRPLRAGRT 456  
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Db 457 LVIPPVMTGMFFVKNVNALAC 477  
RESULT 2  
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C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 04-Feb-2000 #sequence\_revision 04-Feb-2000 #text\_change 09-Jul-2004  
C:Accession: T45608  
R:Bevan, M.; Van Der Schueren, J.; Chuang, Y.J.; Voet, M.; Robben, J.; Volckaert, G.; Ba  
submitted to the Protein Sequence Database, December 1999  
A:Reference number: Z23009  
A:Accession: T45608  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-521 <BEV>  
A:Cross-references: UNIPROT:Q9SDAI; UNIPARC:UPI00000A497C; EMBL:AL133421  
A:Experimental source: cultivar Columbia; BAC clone F13G24  
C:Genetics:  
A:Map position: 5  
A:Introns: 53/3; 66/1; 127/2; 177/1; 256/1; 319/2; 361/2; 394/3  
A:Note: F13G24.30  
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Best Local Similarity 29.2%; Pred. No. 3.4e-23;  
Matches 154; Conservative 68; Mismatches 184; Indels 122; Gaps 24;  
Qy 75 LGSPLKRLTARGLSPAYLRFGGTWTDFLIFPKKKESTFEERSYQSQVNQDICKYGSIPP 134  
Db 55 LTRPLLTAKIKAFKPLRIRIGSLQDQVIYDGNLKT-----PCR----- 94  
Qy 135 DVEEKLRLWEPYQOQLLREHYQKFKNS---TYSRSSV-----DVLTYFANCSGLDLIF 186  
Db 95 -----PFQKM-----NSGLFGFSKGLHMKRWDELNSFLTATGAVVTF 132  
Qy 187 GLNALLRTADLQ-----WNSSNAQLLLDYCSSKGYNI--SWELGNFPNSFLKKAIDIFIN 238  
Db 133 GLNALRGHKLGRKAWGGAWDHINTQDFLNTVSKGYVIDSWERGNELSG--SGVGASVS 190  
Qy 239 GSQLGEDFIQLHKLKLRKSTFNNAKLYGPDVGQP-----RRKTAKMLKSFLKAGGEVIDSV 293  
Db 191 AELYGKDLILVLKDVINK-VYKNSWLHKPILVAPGGFYEQWYTKLLEI---SGPSVVDVV 246  
Qy 294 TWHYYLNGRT--ATREDFLNPDLVDLDFISSQKVF-----QVVESTPGKKVWLGETSSA 347  
Db 247 THHTYNLGSGNDPALVKKIMDPS-----YLSQVSKTFKDVNQTIQEHGFWASPWVSGSGA 302  
Qy 348 YGGGAPLLSDTFAAGFMWLDKLGLSARMGIEWMVRQVFVFGAGNYHLVDE-NFDPLPDYWL 406  
Db 303 YNSGRHVSDTDFIDFWYLDQLGMSARHNTKVYCRQTLVG-GFYGLLEKGTFFVNPDPYS 361  
Qy 407 SLLPFKVLGTVKVLMAVQSGSKRRKRLRVYLHCTNTDNPYKEGDLTLIYAINLHNTKYL-- 464  
Db 362 ALLWHLRMKGVLAVQTDGPP--QLRVYAHCSK-----GRAGVTLLILLNSQSDFTVS 413  
Qy 465 -----RLPYPPFS--NKQVDKYLRLP-----LGPHG--LLSKSVQL 495  
Db 414 VNSGINVVLNAESRKKSLDLTLKRPFSWIGSKASDGYLNRNREYHLTPENGVLRSKTMVL 473  
Qy 496 NGLTKMVDQDTLPPLMEKPLRP--GSSIGLPAFYSFPIVIRNAKVAAC 542  
Db 474 NGKSLKPTATGDIPLS-LPVLRSVNSPLNVLPLSMFSFVLVLPFDASAC 520

RESULT 3  
T01953  
hypothetical protein T2L5.6 - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 26-Feb-1999 #sequence\_revision 26-Feb-1999 #text\_change 09-Jul-2004  
C:Accession: T01953  
R:Geisel, C.; Smith, A.; Le, T.  
submitted to the EMBL Data Library, October 1998  
A:Description: The sequence of A. thaliana T2L5.  
A:Reference number: Z14470  
A:Accession: T01953  
A:Status: translated from GB/EMBL/DDBJ  
A:Molecule type: DNA  
A:Residues: 1-190 <GEI>  
A:Cross-references: UNIPROT:O82604; UNIPARC:UPI00000A08F7D; EMBL:AF096371; NID:g3695386;  
A:Experimental source: cultivar Columbia  
C:Genetics:  
A:Map position: 4  
A:Introns: 36/2; 69/3  
A:Note: T2L5.6  
C:Superfamily: Arabidopsis thaliana hypothetical protein T2L5.6  
Query Match 6.0%; Score 169.5; DB 2; Length 190;  
Best Local Similarity 27.8%; Pred. No. 2.2e-05;  
Matches 54; Conservative 34; Mismatches 57; Indels 49; Gaps 9;  
Qy 382 QVFFFGAGNYHLVD-ENFDPDLPDYWLSLLPFKLVGTVKVLMAVQSGSKRRKRLRVYLHCTNT 440  
Db 12 RQSLIG-GNYGLLNTNTFTNPDPYYSALIRQLMGRKALFTTSGTK--KIRSYTHCA-- 66  
Qy 441 DNPYKEGDLTLIYAINLHNV-----TKYLRLPYPPSNKQVDKYLRLPL 483  
Db 67 ---RQSKG-ITVLLMLNDNTTTVVAKVELNNSFSLRHTKMK-----SYKRASSQLFG-- 115  
Qy 484 GPHGLL-----SKSVQLNGLTLKMWDDQTLPLPMEKPLRPGSSIGLPAFS 528  
Db 116 GPNGVIQREYHLYTAKGNLHSGTMLLGNALQVNSMGDLPPTEPIHINSTEPIIAPYS 175  
Qy 529 YSFFVIIRNAKVAAC 542  
Db 176 IVFVHMENVVVPAC 189  
RESULT 4  
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C:Species: Neurospora crassa  
C:Date: 02-Jun-2000 #sequence\_revision 02-Jun-2000 #text\_change 09-Jul-2004  
R:Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura,  
submitted to the Protein Sequence Database, May 2000  
A:Reference number: Z25022  
A:Accession: T49648  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-2298 <SCH>  
A:Cross-references: UNIPROT:Q96U00; UNIPARC:UPI000017B4BA; EMBL:AL355933; GSPDB:GN00116;  
A:Experimental source: BAC clone B8B20; strain OR74A  
C:Genetics:  
A:Gene: NCSP:B8B20.20  
A:Map position: 6  
A:Introns: 426/3  
Query Match 3.9%; Score 112; DB 2; Length 2298;  
Best Local Similarity 19.3%; Pred. No. 19;  
Matches 114; Conservative 79; Mismatches 190; Indels 208; Gaps 28;  
Qy 78 PKLTLARGLSPA-----YLRFGTGTDFLIFDPKKESTFEERSYQSQV-NQDIC 127  
Db 1447 PRVDLIERLITPSNAHKEACLINIRAWQLARLVVNSGEGSASPRPFTWRNNVFNQILD 1506

Qy 128 KYGSIPTDVEBKLK-----LEWYQEQQLLREHYQKFKKSTYSRSSVDVLYTFAN 178  
Db 1507 QYMAESDIEQOFRALSAENMRSIDAAMREBLITKN-----KATADILHTSAR 1555  
Qy 179 CSGLDLIFGLNAL-----LRTADLQ-----WNSSNAQLLLDYCSSKGYNI 218  
Db 1556 AS-LDVLIKQAKTLEAAIYTLNVTLQKMTTLHFGSGFDGWIILNAL-----DTHAHFL 1609  
Qy 219 SW-ELGNEPNSFLKAGDIFINGSQGBDFIQHKLRLKSTFKNAKLYGPDVGOPRRRTAK 277  
Db 1610 GWIETSSEQYSSNESSADIPRQLEDAILLLQEKLTKEFFWMA-----RELLAL 1659  
Qy 278 MLKSLFKAGGEVID-SVTHHHYILNGRTATREDFLNFDVLDIFISSVQKVPQVVESTPRG 336  
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Qy 369 LGLSAR-MGIEVVMRQVFFGAGNYHL--VDENFDPELDYWLSL-LFKKLVG--TKVL--- 419  
Db 1756 IIKPMRFLGYETYLEAVLQGRGLPFLAEADVSAAGMTPDYNIHLDLFSRAIHYMRKALRG 1815  
Qy 420 -----MASVQGSK-----RRKLRYVYLHCTNTDNPRYKEGDLTLYAINLHNVTXYL 464  
Db 1816 ATTPAPGVTSASTAGSSAQSIIRROREFSH-----1847  
Qy 465 RLPPFSNKQVDKYLRLPLG-----PHCLLSKSVQLNGLTLKMWDD-- 504  
Db 1848 TLQAMTNIRKDLFLRLSLALADPTASTBEHRDYMAFTGLIS-LIKSHGVGIVVDSF 1906  
Qy 505 -----DQTLPLPMKPLRPG-----SSLGLPAPFSYSF-FVIRNAKVA 540  
Db 1907 FLTPSDSYSPLOPQLQHTAGIMAYGVLSEKQVPAASQLFWILFNNEKVA 1957  
RESULT 5  
Tl0666  
hypothetical protein F6E21.40 - Arabidopsis thaliana  
C;Species: Arabidopsis thaliana (mouse-ear cress)  
C;Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 09-Jul-2004  
C;Accession: Tl0666  
R;Bevan, M.; Lennard, N.; Quail, M.; Harris, B.; Rajandream, M.A.; Barrell, B.G.; Bancroft  
submitted to the Protein Sequence Database, June 1999  
A;Reference number: 216533  
A;Accession: Tl0666  
A;Molecule type: DNA  
A;Residues: 1-670 <BBV>  
A;Cross-references: UNIPROT:Q9M090; UNIPARC:UPI000000A4F11; EMBL:AL049914; GSPDB:GN000062;  
A;Experimental source: cultivar Columbia; BAC clone F6E21  
C;Genetics:  
A;Gene: ATSP:F6E21.40  
A;Map position: 4  
A;Introns: 47/3; 123/3; 203/3; 230/2; 255/3; 284/3; 305/1; 335/3; 347/3; 370/3; 39  
C;Superfamily: Schizosaccharomyces pombe negative regulator of mitosis skb1  
Query Match 3.9%; Score 111; DB 2; Length 670;  
Best Local Similarity 22.4%; Pred. No. 3.5;  
Matches 123; Conservative 77; Mismatches 194; Indels 156; Gaps 33;  
Qy 51 LVSPSFLSVTIDANLATDPRFLILGLSGPKLRTLARGSPAY--LRFGGKTDFLIFDPK- 107  
Db 47 LVDESYPPLSVEGN-GVDTQVLPVCGSDLV-----LSPQSWSHVVGKISSWIDLSD 99  
Qy 108 -----KESTPEERSYQSQVNODICKYGSIPDPVEBKLREWPYQQLLRREHYQKFKK 161  
Db 100 EVLRMDSETTLKQEIAMATHLSLQMB-----PD-----LTRPHYLAGGL 139  
Qy 162 NSTYSRSV---DVLY-----TFANCS--GLDLIFGLNALLRTADLQWNSNAQLL 207  
Db 140 RVSCCRSSFISDETFLYKITFNQALTFCGSLFLCNLVALKMLRVLPLVK---SEGDSM 196

Qy 208 LDYCSSKGYNISWELGN-----EPNSFLKKA-DIFIN-----GSQLGEDFTQLHKL 253  
Db 197 DD--TSEGLNDSWELMNSFRLLCEHDSKLSVALDVLSTLPSETSLGRWMGES-VRAAITS 253  
Qy 254 RKSTFNKAKLYGPDVGP--RRKTAKMLKSL-KAGEVIDSVTHHHYILNGRTATREDF 310  
Db 254 TDAFLTNAR-----GYPCUSKRHKQKLIAGFFDHAQAVVICGKPVHNLQKPLDSSSSGTE 307  
Qy 311 LNPDLVDLIDIFISSVQKVPQVVESTPRGKGMWLGSETSSAYGGGAPLLSDTFAAGFMWLDKLG 370  
Db 308 KNP--LRIYLDYVAYLFQKWESELSQEERIELGYRDFLQAPLQPLMDNLEAQTETFE--- 362  
Qy 371 LSARMGIEVVMRQVFFGAGNYHLVDENFDPLPDYWLSSLKFLKVLGVTKVM- 420  
Db 363 ---RDSVKYIQYQ---RAVEKALVDR---VPDEKASEL-----TTVLVVGAGRGPLV 406  
Qy 421 -ASVQGSKR--RKLRYVYLHCTNTDNPRYKEGDLTLYAINLHNVTK-----YLRLPY 468  
Db 407 RASLQAAEETDRKLKVT---AVEKNPN-----AVTTLHNLVKMEGWEDVVTIISCDM 455  
Qy 469 PFNSN--KQVDKYLRLPLGPHGLLSKSVQLNGLTLKMWDDQTLPLM---EKPLRPGSSLG 523  
Db 456 RFWNAPEQADILVSELLGSFG-----DNELSPCEDLGAQRFLKP-DGIS 498  
Qy 524 LPAPSYSFV 533  
Db 499 IPS-SYTSFI 507  
RESULT 6  
S32961  
hypothetical protein YBR259w - yeast (Saccharomyces cerevisiae)  
N;Alternate names: hypothetical protein YBR1727  
C;Species: Saccharomyces cerevisiae  
C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 09-Jul-2004  
C;Accession: S32961; S46140  
R;Doignon, F.; Biteau, N.; Crouzet, M.; Aigle, M.  
Yeast 9, 189-199, 1993  
A;Title: The complete sequence of a 19,482 bp segment located on the right arm of chrom  
A;Reference number: S29348; MUID:93220397; PMID:8465606  
A;Accession: S32961  
A;Status: translation not shown  
A;Molecule type: DNA  
A;Residues: 1-688 <DOI>  
A;Cross-references: UNIPROT:P38338; UNIPARC:UPI000013A298; EMBL:X70529; NID:g1907246; P  
R;Aigle, M.; Baclet, M.C.; Barthe, C.; Bateau, N.; Crouzet, M.; Doignon, F.  
submitted to the Protein Sequence Database, August 1994  
A;Reference number: S45940  
A;Accession: S46140  
A;Molecule type: DNA  
A;Cross-references: UNIPARC:UPI000013A298; EMBL:Z36128; NID:g536684; PIDN:CAA85222.1; P  
C;Genetics:  
A;Cross-references: SGD:S0000463  
A;Map position: 2R  
C;Superfamily: Saccharomyces cerevisiae hypothetical protein YBR259w  
Query Match 3.9%; Score 111; DB 2; Length 688;  
Best Local Similarity 22.5%; Pred. No. 3.6;  
Matches 67; Conservative 45; Mismatches 94; Indels 92; Gaps 16;  
Qy 126 ICKYISPPDVEBKLREWPYQQLLRREHYQKFKKSTYSRSS-----VDVLYT 175  
Db 164 MAYSSNWKWSDDRQLQOFMYEFMRMKLKECLVAFYENFDLQKSSDPLKELIIPWEKIVYV 223  
Qy 176 FANCSGLDLIFGLNALLRTADLQWNSN-----AQLLD-----YCSSKGY----- 216  
Db 224 -ANC--IDAFTGQVRIDGAELIWTSKNLVFSISSAVLRNLNDLQNMFSAPRPYGEALV 280  
Qy 217 -----NLSWELGNFNSFLKKA---DIP--INGSQLG--EDFIQLHKLRLK----- 255  
Db 281 QDFAHIRSLKWSNDKVESLIRALIIFNDMPFYFNKEQVDTKADGIFFLRLLRKFKHEIN 340





RESULT 12  
S00652  
phosphoribosylamine-glycine ligase (EC 6.3.4.13) - fission yeast (*Schizosaccharomyces pombe*)  
N;Alternate names: Aifsase; aminimidazole ribotide synthetase; CARSase; glycylamide rib  
N;Contains: phosphoribosylamine-glycine ligase (EC 6.3.4.13); phosphoribosylformylglycin  
C;Species: *Schizosaccharomyces pombe*  
C;Date: 07-Sep-1990 #sequence\_revision 28-Oct-1994 #text\_change 09-Jul-2004  
C;Accession: S00652; T40496; T40422  
R;McKenzie, R.; Schuchert, P.; Kilbey, B.  
Curr. Genet. 12, 591-597, 1987  
A;Title: Sequence of the bifunctional adel gene in the purine biosynthetic pathway of th  
A;Reference number: S00652; MUID:89003164; PMID:3502942  
A;Accession: S00652  
A;Molecule type: DNA  
A;Residues: 1-788 <MCK>  
A;Cross-references: UNIPROT:P20772; UNIPARC:UPI0000132A3F; EMBL:X06601; NID:G4903; PIDN:  
R;Wood, V.; Rajandream, M.A.; Barrall, B.G.; Lauber, J.; Hilbert, H.; Duesterhoeft, A.  
submitted to the EMBL Data Library, February 1998  
A;Reference number: Z21910  
A;Accession: T40496  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-788 <WOO>  
A;Cross-references: UNIPARC:UPI0000132A3F; EMBL:AL021730; PIDN:CAA16823.1; GSPDB:GN00067  
A;Experimental source: strain 972h; cosmid c4C3  
R;Seeger, K.; Harris, D.; Wood, V.; Rajandream, M.A.; Barrall, B.G.  
submitted to the EMBL Data Library, March 1999  
A;Reference number: Z21928  
A;Accession: T40422  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 604-788 <SEE>  
A;Cross-references: UNIPARC:UPI000016908D; EMBL:AL035655; PIDN:CAB38600.1; GSPDB:GN00067  
A;Experimental source: strain 972h; cosmid c405  
C;Genetics:  
A;Gene: ADEL; SPDB:SPDC405.01  
A;Map position: 2  
C;Superfamily: Saccharomyces cerevisiae ADE5 multifunctional protein; phosphoribosylamin  
C;Keywords: cyclo-ligase; purine nucleotide biosynthesis  
F;5-425/Domain: phosphoribosylamine-glycine ligase homology <PGL>  
F;438-767/Domain: phosphoribosylformylglycinamide cyclo-ligase homology <PFCL>

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Best Local Similarity 27.7%; Pred. No. 13;  
Matches 70; Conservative 36; Mismatches 114; Indels 33; Gaps 11;  
QY 297 HYYLNGRTATRE--DFLNPDV-LDIFISSVQKVFQVVEST-RPGKKWLGTSAY---- 348  
DB 424 HHALNPKRTRREILTYENSGVSDVNGNEFVQRIKDLVKSTRPGADADIGGFGIFDLKQ 483  
QY 349 -GGGAPLL-SDTFAAGFWMLDKGLSAR--MGIEVVMQVFPFAGNHYHLVDENFDPL--P 402  
DB 484 AGWNPDLVSATDGVGSKLLTALSINKHDTVGIDLVANV-----NDLVVQGAEPFLFL 537  
QY 403 DYWLSSLPFKLVGTKVLMAVQSGSKRRKLRYLVHCTNTDNPRYKSGDITLYAINLHNVTK 462  
DB 538 DYFATGSLDLKVSTSFVEGVGKQKQACALVGGTSEMPGLYHDGHYDANGTSVCAVS 597  
QY 463 YLRLLPSPSNKQVDKYLRLPGLPHGLSKSVQLNGTL--KWDV-----DOTLPLMEKPL 516  
DB 598 DDILPKPESFSGKDILL-----GLASDGVHNSNGYSLVRKIVEYSDLEYTSVCPWDKNV 650  
QY 517 RPSGLGLPAFYS 529  
DB 651 RLGDSLLIPTRYI 663

RESULT 13  
F70411  
adenylosuccinate synthetase - Aquifex aeolicus  
C;Species: Aquifex aeolicus

C;Date: 08-May-1998 #sequence\_revision 08-May-1998 #text\_change 09-Jul-2004  
C;Accession: F70411  
R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Oy  
V.

Nature 392, 353-358, 1998  
A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.  
A;Reference number: A70300; MUID:98196666; PMID:9537320  
C;Accession: F70411  
A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-432 <AQF>  
A;Cross-references: UNIPROT:O67321; UNIPARC:UPI00000565A2; GB:AE000733; NID:G2983720; PI  
A;Experimental source: strain VF5  
C;Genetics:  
A;Gene: purA  
C;Superfamily: adenylosuccinate synthase

Query Match 3.7%; Score 104; DB 2; Length 432;  
Best Local Similarity 23.9%; Pred. No. 5.9;  
Matches 96; Conservative 39; Mismatches 128; Indels 138; Gaps 22;  
QY 15 LLLGLPLGSPGALPRPAQADVVLDL-----FFTOEPLHLVSPS 55  
DB 51 ILHLLPTGILHEHVKGVIQGM-VVDLEVLHKEVNLEEKGIYVKERLIFISDRAHLVMPY 109  
QY 56 FLSTVIDANLATDPRFLLILGSPK--LRTLARGLSPAYL-RFGGKTDFLIFDPKKESTF 112  
DB 110 H-----KLLDSUFKKKGIGTTLRGPGPAYMFKYG--RKGIKIRISDLKDEKRF 154  
QY 113 EERSYQSQVNQDICKYSGIPPDVEEK-----LRLEWYPQEQQLLREHYQKKFQNSTY 165  
DB 155 ----YTLEDNLDVFK-----NICEKVFCEKFDLDINQIYEQL----RYFEFKEENV- 199  
QY 166 SRSVDVLYTFPANGSGLDLIFGLNALLRTADL-----QWNSNAQLLDLYCSSKGVNISWE 221  
DB 200 ---VDLLRFPNTQKSVLPBGAQGTLLDDVDMGTYPVYVTSNAGAL-----GLSNG 246  
QY 222 LGNEPNSFLKADIFING-----SQL-GEDFIQLHKLRLKSTFFKNAKLYG 265  
DB 247 TGMPEPKYF---SDAFFLGVAKAYTTRVGEFPFTELKGEKEKUREL-----GGEYG 295  
QY 266 PDVGQPRR---KTAKMLKSFLKAGGEVIDSVTHHHYVINGRTATREDPLNF----- 313  
DB 296 STTGPRRCGWLDLVALKYAVQVNG-----LDGFIKLDVLDTFDEVKVCVA 343  
QY 314 ----DVLIDIFISSVQKVFQV--VESTRPGKKWLGTSAY 347  
DB 344 YELDGEVIDYPPASVSELIRKPVVKTLKG---WKKSTKGA 381

RESULT 14  
D97065  
transketolase [imported] - Clostridium acetobutylicum  
C;Species: Clostridium acetobutylicum  
C;Date: 14-Sep-2001 #sequence\_revision 14-Sep-2001 #text\_change 09-Jul-2004  
C;Accession: D97065  
R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,  
J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.  
J. Bacteriol. 183, 4823-4838, 2001  
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clo  
A;Reference number: A96900; MUID:21359325; PMID:21359325  
A;Accession: D97065  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-796 <KUR>  
A;Cross-references: UNIPROT:Q97JE3; UNIPARC:UPI0000131969; GB:AE001437; PIDN:AAK79311.1;  
A;Experimental source: Clostridium acetobutylicum ATCC824  
C;Genetics:  
A;Gene: CAC1343  
C;Superfamily: phosphoketolase

Query Match 3.7%; Score 104; DB 2; Length 796;  
Best Local Similarity 21.6%; Pred. No. 15;



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GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: February 27, 2006, 17:43:52 ; Search time 234 Seconds  
(without alignments)  
1637.187 Million cell updates/sec

Title: SEQ2-246PHE

Perfect score: 2841

Sequence: 1 MLRSKPALPPPLMLLLGLP.....LPAFSYFFVIRNAKVAACI 543

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt\_05-80:\*

1: uniprot\_sprot:\*

2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2841	100.0	543	2	Q9Y251_HUMAN
2	2834	99.8	543	2	O53GE5_HUMAN
3	2820	99.3	545	2	Q9UL39_HUMAN
4	2285	80.4	545	2	Q9MYX0_BOVIN
5	2153	75.8	535	2	Q8K3K3_MOUSE
6	2143	75.4	535	2	Q6YGI1_MOUSE
7	2138	75.3	536	2	Q71RP1_RAT
8	2126	74.8	536	2	Q9QZF8_RAT
9	1648.5	58.0	523	2	Q90YK5_CHICK
10	1320	46.5	533	2	Q4SYF6_TETNG
11	1150.5	40.5	592	2	Q9HE37_HUMAN
12	1147.5	40.4	592	2	Q5VUH6_HUMAN
13	1142.5	40.2	592	2	Q8WQK2_HUMAN
14	1036.5	36.5	597	2	Q4TB80_TETNG
15	1017.5	35.8	548	2	Q5VUH4_HUMAN
16	1011.5	35.6	548	2	Q8WQK1_HUMAN
17	932.5	32.8	534	2	Q9HE38_HUMAN
18	929.5	32.7	534	2	Q5VUH5_HUMAN
19	893.5	31.5	480	2	Q9HB39_HUMAN
20	742.5	26.1	255	2	Q4TGC8_TETNG
21	699	24.6	515	2	Q8T108_BOMMO
22	417	14.7	521	2	Q9SDA1_ARATH
23	417	14.7	543	2	Q9FF10_ARATH
24	400	14.1	559	2	Q89F99_BRAJA
25	388	13.7	526	2	Q5SNA6_ORYSA
26	379	13.3	541	2	Q691I6_ORYSA
27	377	13.3	527	2	Q9LRC8_SCURA
28	365	12.8	537	2	Q70YJ3_HORVU
29	363	12.8	536	2	Q9FZP1_ARATH
30	353.5	12.4	516	2	Q9FLK8_ARATH
31	353.5	12.4	539	2	Q8L608_ARATH

#### RESULT 1

Q9Y251\_HUMAN  
ID Q9Y251\_HUMAN PRELIMINARY; PRT; 543 AA.  
AC Q9Y251;  
DT 01-NOV-1999 (TrEMBLrel. 12, Created)  
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)  
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)  
DE Heparanase.  
GN Name=HPA; Synonyms=HPSE;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Placenta;  
RX MEDLINE=99321249; PubMed=10395326; DOI=10.1038/10525;  
RA Hulett M.D., Freeman C., Hamdorf B.J., Baker R.T., Harris M.J., Parish C.R.;  
RT "Cloning of mammalian heparanase, an important enzyme in tumor invasion and metastasis.";  
RT Nat. Med. 5:803-809(1999).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RA Vlodavsky I., Friedman Y., Elkin M., Aingorn H., Atzmon R., Ishai-Michaeli R., Bitan M., Pappo O., Peretz T., Michal I., Spector L., Pecker I.;  
RT "Mammalian heparanase: a novel gene involved in tumor progression and metastasis.";  
RT Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Placenta;  
RX MEDLINE=99333379; PubMed=10405343; DOI=10.1006/bbrc.1999.0962;  
RA Kussie P.H., Hulmes J.D., Ludwig D.L., Patel S., Navarro E.C., Seddon A.P., Giorgio N.A., Bohlen P.;  
RT "Cloning and functional expression of a human heparanase gene.";  
RL Biochem. Biophys. Res. Commun. 261:183-187(1999).  
RN [4]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=99377052; PubMed=10446189; DOI=10.1074/jbc.274.34.24153;  
RA Toyoshima M., Nakajima M.;  
RT "Human heparanase. Purification, characterization, cloning, and expression.";  
RL J. Biol. Chem. 274:24153-24160(1999).  
RN [5]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Pancreas;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zengerg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

#### ALIGNMENTS

32	350.5	12.3	529	2	Q6ZJ22_ORYSA	O6zj22	oryza sativ
33	169.5	6.0	190	2	O82604_ARATH	O82604	arabidopsis
34	156	5.5	935	2	Q9VE79_DROME	Q9ve79	drosophila
35	141	5.0	559	2	Q7SEB0_NEUCR	Q7seb0	neurospora
36	138.5	4.9	463	2	Q63T97_BURPS	Q63t97	burkholderi
37	138	4.9	1128	2	Q5TT65_ANOGA	Q5tt65	anopheles g
38	126.5	4.5	493	2	Q9HK01_THEAC	Q9hk01	thermoplasma
39	125.5	4.4	665	2	Q55IC3_CRYNE	Q55ic3	cryptococcus
40	125.5	4.4	665	2	Q5K7V9_CRYNE	Q5k7v9	cryptococcus
41	124	4.4	634	2	Q5NJL7_9BACT	Q5njl7	uncultured
42	124	4.4	765	2	Q4P0C9_USTMA	Q4p0c9	ustilago ma
43	121	4.3	594	2	Q512T2_MAGGR	Q512t2	magnaporthe
44	119	4.2	511	2	Q55MH5_CRYNE	Q55mh5	cryptococcus
45	119	4.2	511	2	Q5K897_CRYNE	Q5k897	cryptococcus

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RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullihy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
[6]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Pancreas;
RA Straubeberg R.;
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
[7]
RP NUCLEOTIDE SEQUENCE.
RA Pinhal M.A., Semedo P.;
RT "Cloned heparanase from MCF-7 cells.";
RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF144325; AAD41342.1; -; mRNA.
DR EMBL; AF152376; AAD45669.1; -; mRNA.
DR EMBL; AF155510; AAD45941.1; -; mRNA.
DR EMBL; AF165154; AAD45379.1; -; mRNA.
DR EMBL; AY948074; AAX47106.1; -; mRNA.
DR EMBL; BC051321; AAH51321.1; -; mRNA.
DR Ensembl; ENSG00000173083; Homo sapiens.
DR GO; GO:0004566; F:beta-glucuronidase activity; TAS.
DR GO; GO:0006029; P:proteoglycan metabolism; TAS.
DR InterPro; IPR005199; Glyco_hydro_79_N.
DR Pfam; PF03662; Glyco_hydro_79n; I.
FT CHAIN 158 543 heparanase.
SQ SEQUENCE 543 AA; 61177 MW; AD262EC267FC4AB2 CRC64;

Query Match 100.0%; Score 2841; DB 2; Length 543;
Best Local Similarity 100.0%; Pred. No. 3.5e-205;
Matches 543; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLLRSKPALPPPLMLLLGPGPLSPGALPRPAQAQDVVDLDFFTQEPHLVSPSFLSVT 60
Db 1 MLLRSKPALPPPLMLLLGPGPLSPGALPRPAQAQDVVDLDFFTQEPHLVSPSFLSVT 60

Qy 61 IDANLATDPRFLILGSPKLTARGLSPAYLRFGGKTDFLI DPDKKESTFEERSYQWS 120
Db 61 IDANLATDPRFLILGSPKLTARGLSPAYLRFGGKTDFLI DPDKKESTFEERSYQWS 120

Qy 121 QVNQDICKYGSIPDPVEEKLREWPYQQLLLREHYQKKFNKSTYSRSSVDVLYTFNACS 180
Db 121 QVNQDICKYGSIPDPVEEKLREWPYQQLLLREHYQKKFNKSTYSRSSVDVLYTFNACS 180

Qy 181 GLDLIFGLNALLRTADLQWNSNAQLLLDYCSSKGYNISWELGNEPNSFLKKADIFINGS 240
Db 181 GLDLIFGLNALLRTADLQWNSNAQLLLDYCSSKGYNISWELGNEPNSFLKKADIFINGS 240

Qy 241 QLGEDFIQLHKLRLKSTFNKAKLYGPDVGQPRRTAKMLKSLFKAGGEVIDSVTWHYYL 300
Db 241 QLGEDFIQLHKLRLKSTFNKAKLYGPDVGQPRRTAKMLKSLFKAGGEVIDSVTWHYYL 300

Qy 301 NGRTATREDFLNPVDLDFISSVQKVFQVVESTREPKKVKWLGETSSAYGGGAPLLSDTFA 360
Db 301 NGRTATREDFLNPVDLDFISSVQKVFQVVESTREPKKVKWLGETSSAYGGGAPLLSDTFA 360

Qy 361 AGFMWLDKLGLSARMGIEVWRQVFPFGAGNTHLVDFNDPDLPDYWLSLFLFKLVGTQKVL 420
Db 361 AGFMWLDKLGLSARMGIEVWRQVFPFGAGNTHLVDFNDPDLPDYWLSLFLFKLVGTQKVL 420

Qy 421 ASVQGSKRRKLRLVYLHCTNTDNPRYKEGDLTLVAINLHNVTKYLRLPYPFSNKQVDKYL 480

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Db 421 ASVQGSKRRKLRLVYLHCTNTDNPRYKEGDLTLVAINLHNVTKYLRLPYPFSNKQVDKYL 480
Qy 481 RPLQPHGLLSKSVOLNGLTLKMVDDQTLPLMEKPLRPGSLGLPAFYSYFFVIRNAKVA 540
Db 481 RPLQPHGLLSKSVOLNGLTLKMVDDQTLPLMEKPLRPGSLGLPAFYSYFFVIRNAKVA 540
Qy 541 ACI 543
Db 541 ACI 543

RESULT 2
Q53GE5_HUMAN
ID Q53GE5_HUMAN PRELIMINARY; PRT; 543 AA.
AC Q53GE5;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Heparanase variant (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Human small intestine;
RA Maruyama K., Sugano S.;
RT "Oligo-capping : a simple method to replace the cap structure of
RT eucaryotic mRNAs with oligoribonucleotides.";
RL Gene 138:171-174 (1994).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Human small intestine;
RA Suzuki Y., Yoshitomo K., Maruyama K., Suyama A., Sugano S.;
RT "Construction and characterization of a full length-enriched and a 5'-
RT end-enriched cDNA library.";
RL Gene 200:149-156 (1997).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Human small intestine;
RA Suzuki Y., Sugano S., Totoki Y., Toyoda A., Takeda T., Sakaki Y.,
RA Tanaka A., Yokoyama S.;
RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
FT EMBL; AK222986; BAD96706.1; -; mRNA.
FT NON_TER 1
SQ SEQUENCE 543 AA; 61118 MW; AC392EC267FC4AB2 CRC64;

Query Match 99.8%; Score 2834; DB 2; Length 543;
Best Local Similarity 99.8%; Pred. No. 1.2e-204;
Matches 542; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MLLRSKPALPPPLMLLLGPGPLSPGALPRPAQAQDVVDLDFFTQEPHLVSPSFLSVT 60
Db 1 MLLRSKPALPPPLMLLLGPGPLSPGALPRPAQAQDVVDLDFFTQEPHLVSPSFLSVT 60

Qy 61 IDANLATDPRFLILGSPKLTARGLSPAYLRFGGKTDFLI DPDKKESTFEERSYQWS 120
Db 61 IDANLATDPRFLILGSPKLTARGLSPAYLRFGGKTDFLI DPDKKESTFEERSYQWS 120

Qy 121 QVNQDICKYGSIPDPVEEKLREWPYQQLLLREHYQKKFNKSTYSRSSVDVLYTFNACS 180
Db 121 QVNQDICKYGSIPDPVEEKLREWPYQQLLLREHYQKKFNKSTYSRSSVDVLYTFNACS 180

Qy 181 GLDLIFGLNALLRTADLQWNSNAQLLLDYCSSKGYNISWELGNEPNSFLKKADIFINGS 240
Db 181 GLDLIFGLNALLRTADLQWNSNAQLLLDYCSSKGYNISWELGNEPNSFLKKADIFINGS 240

Qy 241 QLGEDFIQLHKLRLKSTFNKAKLYGPDVGQPRRTAKMLKSLFKAGGEVIDSVTWHYYL 300
Db 241 QLGEDFIQLHKLRLKSTFNKAKLYGPDVGQPRRTAKMLKSLFKAGGEVIDSVTWHYYL 300

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QY 301 NGRATATREDFLNPVDLIDIFISSVQKVFQVVESTTRPGKVKWLGWLTSSAYGGGAPLLSDTFA 360
DB 301 NGRATATREDFLNPVDLIDIFISSVQKVFQVVESTTRPGKVKWLGWLTSSAYGGGAPLLSDTFA 360
QY 361 AGFWMLDKLGLSARMGLGVVMRQVFFGAGNHYHLDENFDPLPDYWLSSLFKKLVTGTVLM 420
DB 361 AGFWMLDKLGLSARMGLGVVMRQVFFGAGNHYHLDENFDPLPDYWLSSLFKKLVTGTVLM 420
QY 421 ASVQSGSKRRKLRVYLHCTNTDNPRYKEGDLTLYAINLHNVTYKLRLLPYFSPNKKQVDKYL 480
DB 421 ASVQSGSKRRKLRVYLHCTNTDNPRYKEGDLTLYAINLHNVTYKLRLLPYFSPNKKQVDKYL 480
QY 481 RPLGPHGLLSKSVQLNGLTLKQVDDQTLPLMEKPLRPGSSGLGPAFYSFFVIRNAKVA 540
DB 481 RPLGPHGLLSKSVQLNGLTLKQVDDQTLPLMEKPLRPGSSGLGPAFYSFFVIRNAKVA 540
QY 541 ACI 543
DB 541 ACI 543

RESULT 3
Q9UL39_HUMAN
ID Q9UL39_HUMAN PRELIMINARY; PRT; 545 AA.
AC Q9UL39;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Heparanase.
GN Name=HPSE;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Placenta;
RX MEDLINE=20229546; PubMed=10764835; DOI=10.1093/glycob/10.5.467;
RA Dempsey L.A., Plummer T.B., Coombes S.L., Platt J.L.;
RT "Heparanase expression in invasive trophoblasts and acute vascular
RT damage."
RL Glycobiology 10:467-475 (2000).
DR EMBL; AF084467; AAD54516.1; -; mRNA.
DR Ensembl; ENSG00000173083; Homo sapiens.
DR HGNC; HGNC:5164; HPSE.
DR InterPro; IPR005199; Glyco_hydro_79N.
DR Pfam; PF03662; Glyco_hydro_79n; 1.
DR TrEMBL; P03662; Glyco_hydro_79n; 1.
SQ SEQUENCE 545 AA; 61417 MW; 67B80ACD73C5A9A1 CRC64;

Query Match 99.3%; Score 2820; DB 2; Length 545;
Best Local Similarity 99.6%; Pred. No. 1.4e-203;
Matches 543; Conservative 0; Mismatches 0; Indels 2; Gaps 2;

QY 1 MLLRSKPPALPPP-LMLLLGLPLGSPGALPRPAQA-QDVVDLDFFTQEPHLHVSFSL 58
DB 1 MLLRSKPPALPPP-LMLLLGLPLGSPGALPRPAQAQDVVDLDFFTQEPHLHVSFSL 60
QY 59 VTIDANLATDPRFLILGSPKRLTLARGLSPAYLRFGGTKTDFLI FDPKKESTFEERSY 118
DB 61 VTIDANLATDPRFLILGSPKRLTLARGLSPAYLRFGGTKTDFLI FDPKKESTFEERSY 120
QY 119 OSQVQNDICKYGSIPDPVEKRLWEYPQQLLREHYQKKFNKSTYSRSSVDVLYTFAN 178
DB 121 OSQVQNDICKYGSIPDPVEKRLWEYPQQLLREHYQKKFNKSTYSRSSVDVLYTFAN 180
QY 179 CSGLDLIFGLNALLRTADLQWNSNAQLLLDYCSSKGYNISWELGNEPNSFLKKADIFIN 238
DB 181 CSGLDLIFGLNALLRTADLQWNSNAQLLLDYCSSKGYNISWELGNEPNSFLKKADIFIN 240
QY 239 GSQLGEDFIQLHLKLRKSTFKNAKLYGPDVGQPRRTAKMLKSFLLKAGGEVIDSVTWHY 298
DB 241 GSQLGEDFIQLHLKLRKSTFKNAKLYGPDVGQPRRTAKMLKSFLLKAGGEVIDSVTWHY 300

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QY 299 YLNGRTATREDFLNPVDLIDIFISSVQKVFQVVESTTRPGKVKWLGWLTSSAYGGGAPLLSDT 358
DB 301 YLNGRTATREDFLNPVDLIDIFISSVQKVFQVVESTTRPGKVKWLGWLTSSAYGGGAPLLSDT 360
QY 359 FAAGFWMLDKLGLSARMGLGVVMRQVFFGAGNHYHLDENFDPLPDYWLSSLFKKLVTGTV 418
DB 361 FAAGFWMLDKLGLSARMGLGVVMRQVFFGAGNHYHLDENFDPLPDYWLSSLFKKLVTGTV 420
QY 419 LMASVQSGSKRRKLRVYLHCTNTDNPRYKEGDLTLYAINLHNVTYKLRLLPYFSPNKKQVDK 478
DB 421 LMASVQSGSKRRKLRVYLHCTNTDNPRYKEGDLTLYAINLHNVTYKLRLLPYFSPNKKQVDK 480
QY 479 LLRLPGLGHLLSKSVQLNGLTLKQVDDQTLPLMEKPLRPGSSGLGPAFYSFFVIRNAK 538
DB 481 LLRLPGLGHLLSKSVQLNGLTLKQVDDQTLPLMEKPLRPGSSGLGPAFYSFFVIRNAK 540
QY 539 VAACI 543
DB 541 VAACI 545

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## RESULT 4

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Q9MYI0_BOVIN
ID Q9MYI0_BOVIN PRELIMINARY; PRT; 545 AA.
AC Q9MYI0;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Heparanase.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Placenta;
RX MEDLINE=21176669; PubMed=11277877;
RA Kizaki K., Nakano H., Nakano H., Takahashi T., Imai K., Hashizume K.;
RT "Expression of heparanase mRNA in bovine placenta during gestation."
RL Reproduction 121:573-580 (2001).
DR EMBL; AF281160; AAF87301.2; -; mRNA.
DR InterPro; IPR005199; Glyco_hydro_79N.
DR Pfam; PF03662; Glyco_hydro_79n; 1.
DR TrEMBL; P03662; Glyco_hydro_79n; 1.
SQ SEQUENCE 545 AA; 61076 MW; FAC4BDFD855B933 CRC64;

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Query Match 80.4%; Score 2285; DB 2; Length 545;  
 Best Local Similarity 80.0%; Pred. No. 2.8e-163;  
 Matches 436; Conservative 34; Mismatches 73; Indels 2; Gaps 1;

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QY 1 MLLRSKPPALPPP-LMLLLGLPLGSPGALPRPAQAQDVVDLDFFTQEPHLHVSFSL 58
DB 1 MLLRSKPPALPPP-LMLLLGLPLGSPGALPRPAQAQDVVDLDFFTQEPHLHVSFSL 60
QY 59 VTIDANLATDPRFLILGSPKRLTLARGLSPAYLRFGGTKTDFLI FDPKKESTFEERSY 118
DB 61 VTIDANLATDPRFLILGSPKRLTLARGLSPAYLRFGGTKTDFLI FDPKKESTFEERSY 120
QY 119 OSQVQNDICKYGSIPDPVEKRLWEYPQQLLREHYQKKFNKSTYSRSSVDVLYTFAN 178
DB 121 OSQVQNDICKYGSIPDPVEKRLWEYPQQLLREHYQKKFNKSTYSRSSVDVLYTFAN 180
QY 179 CSGLDLIFGLNALLRTADLQWNSNAQLLLDYCSSKGYNISWELGNEPNSFLKKADIFIN 238
DB 181 CSGLDLIFGLNALLRTADLQWNSNAQLLLDYCSSKGYNISWELGNEPNSFLKKADIFIN 240
QY 239 GSQLGEDFIQLHLKLRKSTFKNAKLYGPDVGQPRRTAKMLKSFLLKAGGEVIDSVTWHY 298
DB 241 GSQLGEDFIQLHLKLRKSTFKNAKLYGPDVGQPRRTAKMLKSFLLKAGGEVIDSVTWHY 300
QY 299 YLNGRTATREDFLNPVDLIDIFISSVQKVFQVVESTTRPGKVKWLGWLTSSAYGGGAPLLSDT 358
DB 301 YLNGRTATREDFLNPVDLIDIFISSVQKVFQVVESTTRPGKVKWLGWLTSSAYGGGAPLLSDT 360

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Db 301 YVNGRIATKEDFLNPDILDTFISSVQKTRIVEKIRPLKVKWLGETSSAFGGGAPFLSNT 360  
QY 359 FAAGFMWLDKGLSARMGIEVVMROVFGAGNYHLVDENFPLPDYWLILFLPKLVGTKV 418  
Db 361 FAAGFMWLDKGLSARMGIEVVMROVLFPGAGNYHLVDGNFPLPDYWLILFLPKLVGNKV 420  
QY 419 LMASVQGSKRKRRLRVLYLHCTNTDNPYKREGDLTYAIALNHNVTYKLRPFPSNKNQVDKY 478  
Db 421 LMASVKGPDRSKFRVYLHCTNTKHPRYKREGDLTYALNHNVTYKLELPHFLFNKQVDKY 480  
QY 479 LLRPLGPHGLSKSVQLNGLTLKMVDQDTLPLPMEKPLRPSSGLGPAFYSFFVIRNAK 538  
Db 481 LIKPSGTDLGLSKSVQLNGOILKMVDEQTLPALTEKPLHPGSSLCMPFPFSYGFVIRNAK 540  
QY 539 VAACI 543  
Db 541 VAACI 545

RESULT 5  
QBK3K3 MOUSE  
ID QBK3K3 MOUSE PRELIMINARY; PRT; 535 AA.  
AC QBK3K3;  
DT 01-OCT-2002 (TReMBLrel. 22, Created)  
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)  
DT 01-FEB-2005 (TReMBLrel. 29, Last annotation update)  
DE Heparanase (Mus musculus 0 day neonate thymus cDNA, RIKEN full-length  
DE enriched library, clone:A43010M04 product:heparanase, full insert  
DE sequence).  
GN Name=Hps; Synonyms=Hpa, Hspe;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muridae; Murinae; Mus.  
OX NCBI TaxID=10090;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=FVB;  
RX Miao H.-Q., Navarro E., Patel S., Sargent D., Koo H., Wan H.,  
RA Plata A., Zhou Q., Ludwig D., Bohlen P., Kussie P.;  
RT "Cloning, expression, and purification of mouse heparanase.";  
RL Protein Expr. Purif. 0:0-0(2002).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J; TISSUE=Thymus;  
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;  
RA Carninci P., Hayashizaki Y.;  
RT "High-efficiency full-length cDNA cloning.";  
RL Meth. Enzymol. 303:19-44(1999).  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J; TISSUE=Thymus;  
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;  
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,  
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yananaka I.,  
RA Saito K., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,  
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,  
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,  
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,  
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,  
RA Blake J., Boffelli D., Bojunga C., Carninci P., de Bonaldo M.F.,  
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,  
RA Gustincich S., Hall D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,  
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,  
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,  
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,  
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohtsuki S.,  
RA Hayashizaki Y.;  
RT "Functional annotation of a full-length mouse cDNA collection.";  
RL Nature 409:685-690(2001).

RN NUCLEOTIDE SEQUENCE.  
RP STRAIN=C57BL/6J; TISSUE=Thymus;  
RX MEDLINE=22354683; PubMed=12468851; DOI=10.1038/nature01266;  
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,  
RA Nikaide I., Osato N., Saito R., Suzuki H., Yananaka I., Kiyosawa H.,  
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,  
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,  
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,  
RA Blake J.A., Bradt D., Brusic V., Chohtia C., Corbani L.E., Cousins S.,  
RA Dalla E., Dragan T.A., Fletcher C.F., Forrest A., Frazer K.L.S.,  
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,  
RA Grimmer S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,  
RA Kanai A., Kawai H., Kawasawa Y., Kedzierski R.M., King B.L.,  
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,  
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,  
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,  
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,  
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,  
RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,  
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,  
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,  
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,  
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,  
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,  
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,  
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,  
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,  
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,  
RA Birney E., Hayashizaki Y.;  
RT "Analysis of the mouse transcriptome based on functional annotation of  
RT 60,770 full-length cDNAs.";  
RL Nature 420:563-573(2002).  
RN [5]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J; TISSUE=Thymus;  
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;  
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,  
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;  
RT "Normalization and subtraction of cap-trapper-selected cDNAs to  
RT prepare full-length cDNA libraries for rapid discovery of new genes.";  
RL Genome Res. 10:1617-1630(2000).  
RN [6]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J; TISSUE=Thymus;  
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;  
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,  
RA Konno H., Akiyama J., Nishi K., Kitsuunai T., Tashiro H., Itoh M.,  
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,  
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kaehiwagi K.,  
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,  
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,  
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;  
RT "RIKEN integrated sequence analysis (RISA) system-384-format  
RT sequencing pipeline with 384 multicapillary sequencer.";  
RL Genome Res. 10:1757-1771(2000).  
RN [7]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J; TISSUE=Thymus;  
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;  
RA Adachi J., Aizawa K., Akimura T., Hara A., Hashizume W.,  
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,  
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,  
RA Kato H., Kawai J., Kojima Y., Itoh M., Kagawa I., Kasukawa T.,  
RA Kori F., Imotani K., Ishii Y., Itoh M., Kondo S., Konno H., Koya S.,  
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,  
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,  
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,  
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,  
RA Tagawa A., Takanashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,  
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;  
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
RN [8]  
RP NUCLEOTIDE SEQUENCE.

RESULT	7	Q71RP1_RAT	PRELIMINARY;	PRT;	536 AA.
ID	Q71RP1_RAT				
AC	Q71RP1;				
DT	05-JUL-2004	(T-EMBLrel. 27, Created)			
DT	05-JUL-2004	(T-EMBLrel. 27, Last sequence update)			
DT	05-JUL-2004	(T-EMBLrel. 27, Last annotation update)			
DE	Heparanase.				
GN	Name:Hps; Synonym:Hsape;				
OS	Rattus norvegicus (Rat)				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;				
OC	Muridae; Murinae; Rattus.				
NCBI_TaxID=10116;					
[1]					
NR	NCBIOTIDE SEQUENCE.				
RP					
RA	Rulett M.D., Wang J., Hornby J.R., Freeman C., Pagler E., McHenry J., Parish C.R.;				

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RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF359508; AAQ15189.1; -, mRNA.
DR RGD; 61969; Hpse.
DR InterPro; IPR005199; Glyco_hydro_79N.
DR Pfam; PF03662; Glyco_hydro_79n; 1.
SQ SEQUENCE 536 AA; 60479 MW; C434E04CF536EA4D CRC64;

Query Match 75.3%; Score 2138; DB 2; Length 536;
Best Local Similarity 76.3%; Pred. No. 3.2e-152;
Matches 408; Conservative 49; Mismatches 78; Indels 0; Gaps 0;

Qy 9 LPPPLMLLLGPGSPGALPRPAQAQDVVDLDFFTQEPHLVSPSPFLSVTTIDANLATD 68
Db 2 LRPLLLWLWGRALALTOGTAGTAPTKDVVDLEFYTKRLFQSPSPFLSVTTIDASLATD 61
Qy 69 PRFLLILGSPKLRTLARGLSPAYLRFGGTKTDFLIFDPKKESTFEERSYQSQVNQDICK 128
Db 62 PRFLTFLGSPRLRALARGLSPAYLRFGGTKTDFLIFDPNKEPTSEERSYQSQVNNDICG 121
Qy 129 YGSIPTDVEEKLRLWPYQEQILLREHYQKFKNSTYSRSSVDVLYTFANCGLDLIFGL 188
Db 122 SERVADVLRLKQWEPFQELLRLREYQREFKNSTYSRSSVDMLYSFAKSRDLIFGL 181
Qy 189 NALLRTADLWNSSNAQLLLDYCSSKGYNISWELGNPNFLKKADIFINGSQLGEDFIQ 248
Db 182 NALLRTDPLRNSSNAQLLLNYCSSKGYNISWELGNPNFSFKKAHISIDGLQGEDFVE 241
Qy 249 LHLLRKSTFKNAKLYGPDVGQPRRTAKMLKSLFKAGGEVIDSVTHHHYVINGRTATRE 308
Db 242 LHLLQKSAFQNAKLYGPDIGOPRGKTVKLLRSFLKAGGEVIDSLTWHHHYVINGRVATKE 301
Qy 309 DFLNPVDLVDIFISSQVKVQFVVESTPGKKVWLGETSSAYGGAPLLSDTFAAGFMWLDK 368
Db 302 DFLSSDVLDTFILSVQKILVKTKEMTPGKKVWLGETSSAYGGAPLLSNTPAAGFMWLDK 361
Qy 369 LGLSARMGIEVVMRQVFFGAGNYHLVDENPDPLDYWLSLLFKLVGPKVLMASVQSGKR 428
Db 362 LGLSAQLGIEVVMRQVFFGAGNYHLVDENPEPLDYWLSLLFKLVGPKVLMASVQSGPDR 421
Qy 429 RKLRYLHCTNTDNPYKEGDLTYAHLNHNVTYRLPYPPFSNKQVDKYLLRPLGPHGL 488
Db 422 SKLRVYLHCTNVHPYRREGDLTYVNLNHNVTYKHLKLPMPFSPRPVDKYLLKPFSGDGL 481
Qy 489 LSKSVQLNGTLKMWDDQTLPLMEKPLRPGSSSLGPAFYSFFVIRNAKVAACI 543
Db 482 LSKSVQLNGQTLKMWDEQTLPALTEKPLPAGSSLSVPAPSYGFFVIRNAKIAACI 536

RESULT 8
Q9QZF8_RAT PRELIMINARY; PRT; 536 AA.
AC Q9QZF8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Heparanase.
GN Name=Hpse; Synonyms=Hep;
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22194309; PubMed=12077130; DOI=10.1074/jbc.M203282200;
RA Podyma-Inoue K.A., Yokote H., Sakaguchi K., Ikuta M., Yanagishita M.;
RT "Characterization of heparanase from a rat parathyroid cell line.";
RL J. Biol. Chem. 277:32459-32465 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Podyma K.A., Yokote H., Sakaguchi K., Ikuta M., Yanagishita M.;
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF184967; AAF04563.1; -, mRNA.
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DR RGD; 61969; Hpse.
DR InterPro; IPR005199; Glyco_hydro_79N.
DR Pfam; PF03662; Glyco_hydro_79n; 1.
SQ SEQUENCE 536 AA; 60568 MW; 6208B1FD9EB28421 CRC64;

Query Match 74.8%; Score 2126; DB 2; Length 536;
Best Local Similarity 75.9%; Pred. No. 2.6e-151;
Matches 406; Conservative 50; Mismatches 79; Indels 0; Gaps 0;

Qy 9 LPPPLMLLLGPGSPGALPRPAQAQDVVDLDFFTQEPHLVSPSPFLSVTTIDANLATD 68
Db 2 LRPLLLWLWGRALALTOGTAGTAPTKDVVDLEFYTKRLFQSPSPFLSVTTIDASLATD 61
Qy 69 PRFLLILGSPKLRTLARGLSPAYLRFGGTKTDFLIFDPKKESTFEERSYQSQVNQDICK 128
Db 62 PRFLTFLGSPRLRALARGLSPAYLRFGGTKTDFLIFDPNKEPTSEERSYQSQVNNDICG 121
Qy 129 YGSIPTDVEEKLRLWPYQEQILLREHYQKFKNSTYSRSSVDVLYTFANCGLDLIFGL 188
Db 122 SERVADVLRLKQWEPFQELLRLREYQREFKNSTYSRSSVDMLYSFAKSRDLIFGL 181
Qy 189 NALLRTADLWNSSNAQLLLDYCSSKGYNISWELGNPNFLKKADIFINGSQLGEDFIQ 248
Db 182 NALLRTDPLRNSSNAQLLLNYCSSKGYNISWELGNPNFSFKKAQISIDGLQGEDFVE 241
Qy 249 LHLLRKSTFKNAKLYGPDVGQPRRTAKMLKSLFKAGGEVIDSVTHHHYVINGRTATRE 308
Db 242 LHLLQKSAFQNAKLYGPDIGOPRGKTVKLLRSFLKAGGEVIDSLTWHHHYVINGRVATKE 301
Qy 309 DFLNPVDLVDIFISSQVKVQFVVESTPGKKVWLGETSSAYGGAPLLSDTFAAGFMWLDK 368
Db 302 DFLSSDVLDTFILSVQKILVKTKEMTPGKKVWLGETSSAYGGAPLLSNTPAAGFMWLDK 361
Qy 369 LGLSARMGIEVVMRQVFFGAGNYHLVDENPDPLDYWLSLLFKLVGPKVLMASVQSGKR 428
Db 362 LGLSAQLGIEVVMRQVFFGAGNYHLVDENPEPLDYWLSLLFKLVGPKVLMASVQSGPDR 421
Qy 429 RKLRYLHCTNTDNPYKEGDLTYAHLNHNVTYRLPYPPFSNKQVDKYLLRPLGPHGL 488
Db 422 SKLRVYLHCTNVHPYRREGDLTYVNLNHNVTYKHLKLPMPFSPRPVDKYLLKPFSGDGL 481
Qy 489 LSKSVQLNGTLKMWDDQTLPLMEKPLRPGSSSLGPAFYSFFVIRNAKVAACI 543
Db 482 LSKSVQLNGQTLKMWDEQTLPALTEKPLPAGSSLSVPAPSYGFFVIRNAKIAACI 536

RESULT 9
Q9QYK5_CHICK PRELIMINARY; PRT; 523 AA.
AC Q9QYK5;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Heparanase.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21369959; PubMed=11387326; DOI=10.1074/jbc.M102462200;
RA Goldschmidt O., Zcharia E., Aingorn H., Guatta-Rangini Z., Azmon R.,
RA Michal I., Pecker I., Mitrani E., Vlodavsky I.;
RT "Expression pattern and secretion of human and chicken heparanase are
determined by their signal peptide sequence.";
RL J. Biol. Chem. 276:29178-29187 (2001).
DR EMBL; AY037007; AAK82648.1; -, mRNA.
DR Ensembl; ENSGALG0000011203; Gallus gallus.
DR InterPro; IPR005199; Glyco_hydro_79N.
DR Pfam; PF03662; Glyco_hydro_79n; 1.
SQ SEQUENCE 523 AA; 58386 MW; 85B0B7B18C9BF881 CRC64;
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Query Match 58.0%; Score 1648.5; DB 2; Length 523;  
 Best Local Similarity 60.3%; Pred. No. 2.4e-115;  
 Matches 321; Conservative 86; Mismatches 114; Indels 11; Gaps 3;

QY 13 LMLLLGLPLSPALPRPAQAQDVVDLDFFTQEPHLVSPSPFLSVTTIDANLATDPRFL 72  
 DB 2 LVLLLLVLLAVPP-----RTAEQLQGLREPAGVSPAPSLUTLQASLARDPRFV 52  
 QY 73 ILLGSPKLRTLARGSPAYLRFGGTKTDFLIFDPKKESTFEERSYQSQVNQDICKYGS 132  
 DB 53 ALLRHPKLTLAGSLSPGLRFGGTSTDFLIFNPKDSTWEEKVLSFQA-KOVCEAWPS 111  
 QY 133 PPVVEEKLRLWPQOEQLLREHVKQKPKNSTYSSRSVDVLYTFANCGLDLIFGLNALL 192  
 DB 112 FAVVPKLLLTQWPLQEKLLAEHSWKHKNTTITRSTLDILHTPASSSGFRLVFLNALL 171  
 QY 193 RTADLQWSSNAQLLDYCSSKYNISWELGNEPNSFKKADIFINGSOLGCEPIQLHLK 252  
 DB 172 RRAGLQWSSNAQLLDYCSSKYNISWELGNEPNSFKKADIFINGSOLGCEPIQLHLK 231  
 QY 253 L-RKSTFNKAKLYGPDVGPQRRKTAQMLKSPKAGGVEIDSVTWHHYLNGRTATREDFL 311  
 DB 232 LSQHPLYRHAELYGLDVGPQRRKTAQMLKSPKAGGVEIDSVTWHHYLNGRTATREDFL 291  
 QY 312 NPQVLDIFISVQKVFQVVESTTRPGKVKWLGESTSSAYGGGAPLSDTFAAGFMWLDKGL 371  
 DB 292 SPEVLDSPATAIHDLVGLIVEATVPKKVWLGESTSSAYGGGAPLSDTFAAGFMWLDKGL 351  
 QY 372 SARNGIEVWROVFPGAGNHYLDENFDPLDYHLSLLFKLVCTKVLMAVQSGSKRL 431  
 DB 352 AARGIDVWROVFPGAGNHYLDENFDPLDYHLSLLFKLVCTKVLMAVQSGSKRL 411  
 QY 432 RVYLHCTNTONPRYKEGDLTYAINLHNVTYLPFNSKQVDKYLRLPLGPHGLLSK 491  
 DB 412 RVYLHCTNPRPKYREGDVTLPALNSVTSQSLQPKQLSKSVQDQVLLPHGKDSILSR 471  
 QY 492 SVQLNGLTLKQVDDQTLPLMEKPLRPGSSGLGPAFYSFFVIRNAKVAACI 543  
 DB 472 EVQLNGRLQLQWDDQTLPLMEKPLRPGSSGLGPAFYSFFVIRNAKVAACI 523

RESULT 10  
 Q4SYF6\_TETNG  
 ID Q4SYF6\_TETNG PRELIMINARY; PRT; 533 AA.  
 AC Q4SYF6;  
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)  
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)  
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)  
 DE Chromosome undetermined SCAF12073, whole genome shotgun sequence.  
 DE (Fragment).  
 GN ORFNames=GSTENG0010356001;  
 OS Tetraodon nigroviridis (Green puffer).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
 OC Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;  
 OC Tetraodontidae; Tetraodontidae; Tetraodon.  
 OX NCBI\_TaxID=99883;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Jallou O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,  
 RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,  
 RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,  
 RA Dailly C., Salanoubat M., Levy M., Boudet N., Castellano S.,  
 RA Anthonard V., Jubin C., Castelli V., Katinka M., Vacherie B.,  
 RA Blemont C., Skalli Z., Cattolico L., Poullain J., De Bernardis V.,  
 RA Cruaud C., Duprat S., Brottier C., Coutanceau J.P., Gouzy J.,  
 RA Parra G., Lardier G., Chapelle C., McKernan K.J., McEwan P., Bosak S.,  
 RA Kellis M., Wolff J.N., Guigo R., Zody M.C., Mesirov J.,  
 RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,  
 RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,  
 RA Winkler P., Lander E.S., Weissbach J., Roest Crolius H.,  
 RA "Genome duplication in the teleost fish Tetraodon nigroviridis reveals  
 RT the early vertebrate proto-karyotype."

Nature 431:946-957 (2004).  
 [2]  
 RL NUCLEOTIDE SEQUENCE.  
 RN Genoscope: Whitehead Institute Centre for Genome Research;  
 RG Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.  
 CC -1- CAUTION: The sequence shown here is derived from an  
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
 CC preliminary data.  
 CC EMBL; CAAE01012073; CAF94326.1; -; Genomic\_DNA.  
 DR NON\_TER 1 1  
 FT NON\_TER 533 533  
 SQ SEQUENCE 533 AA; 60100 MW; 9B00A7C8780100FF CRC64;  
 Query Match 46.5%; Score 1320; DB 2; Length 533;  
 Best Local Similarity 50.2%; Pred. No. 1.4e-90;  
 Matches 269; Conservative 82; Mismatches 141; Indels 44; Gaps 8;

QY 49 LHLVSPFLSVTTIDANLATDPRFLILGSPKLTARGLSPAYLRFGGTKTDFLIFPKK 108  
 DB 1 LRRVDFRFLSVTTIDASLAADERFMYLLSSPKVTLAKALTAPFLRFGTQDFMVFAPHK 60  
 QY 109 E---STFEERSYQSQVNQDICKYGSITPPDVEEKLRLWEPYQQLLREHYOKFKNSTY 165  
 DB 61 NQASGFSARELTFSSNGHSCCKMAPPWLERRLRTEMKQOVMLRNESELQRYRVKF 120  
 QY 166 SRSSVDVLYTFANCGLDLIFGLNALLRTADLQWSSNAQLLDYCSSKYNISWELGNE 225  
 DB 121 TETTVQHLAFANCGLDLVFLNALLRTADLQWSSNAQLLDYCSSKYNISWELGNE 180  
 QY 226 PNSFLKAKKADIFINGSOLGCEPIQLHLKLRKSTF-KNAKLYGPDVGPQRRKTAQMLSKFLK 284  
 DB 181 PNSYEKAGLRLDGRQLGDEFTVLRKTLRESREYRDAGLFGPDVGPQRRKIDILSGFLQ 240  
 QY 285 AGGEVDSVTWHHYLNGRTATREDFLNPDVLDIFISVQKVFQVVESTTRPGKVKWLGEST 344  
 DB 241 SGAEVADACTWHHYLNGRTATREDFLNPDVLDIFISVQKVFQVVESTTRPGKVKWLGEST 300  
 QY 345 SSAYGGGAPLSDTFAAGFMWLDKGLSARMGTEVWROVFPGAGNHYLDENFDPLP-- 402  
 DB 301 SSAYGGGAGLSDTFAAGFMWLDKGLSARMGTEVWROVFPGAGNHYLDENFDPLP-- 360  
 QY 403 -----DYWLSLLPKLVGTVKVLMA-----SVQSGKRRLRVYLHCTNTDN----- 442  
 DB 361 GLLLDQYWLSSLYKLVGQEVLTTRTPGPAGSER--VRLYLHCANKQRCSSLLQLFLSVRK 418  
 QY 443 -----PRYKEGDLTYAINLHNVTYLPFNSKQVDKYLRL--RPLGPHG 487  
 DB 419 QRKEARFSLVSLCSYRSGAATLMSNLSKQAPARISLPRILSSSTVFAVLESQD-GE 477  
 QY 488 LLSKSYQLNGLTLKQVDDQTLPLMEKPLRPGSSGLGPAFYSFFVIRNAKVAACI 543  
 DB 478 LRSRAVKLNGRLVWDDQTLPLMEKPLRPGSSGLGPAFYSFFVIRNAKVAACI 533

RESULT 11  
 Q9HB37\_HUMAN  
 ID Q9HB37\_HUMAN PRELIMINARY; PRT; 592 AA.  
 AC Q9HB37;  
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE Hepatanase-like protein HPA2c.  
 OS Homo sapiens (human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;  
 OC Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA MEDLINE-20483645; PubMed-11027606; DOI=10.1006/bbrc.2000.3586;  
 RA McKenzie E., Tyson K., Stamps A., Smith P., Turner P., Barry R.,  
 RA Hircok M., Patel S., Barry E., Stubbfield C., Terrett J., Page M.,  
 RT "Cloning and expression profiling of Hpa2, a novel mammalian









Job time : 236 secs



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GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: February 27, 2006, 17:43:32 ; Search time 188 Seconds  
(without alignments)  
1269.057 Million cell updates/sec

Title: SEQ2-246PHE

Perfect score: 2841

Sequence: 1 MLRSKPALEPPPLMLLLGP.....LPAFSYFFVIRNAKAAACI 543

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

A Geneseq\_21:\*

- 1: geneseqp1980s:\*
- 2: geneseqp1990s:\*
- 3: geneseqp2000s:\*
- 4: geneseqp2001s:\*
- 5: geneseqp2002s:\*
- 6: geneseqp2003as:\*
- 7: geneseqp2003bs:\*
- 8: geneseqp2004s:\*
- 9: geneseqp2005s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2841	100.0	543	2 AAY17082	Aay17082 Human hep
2	2841	100.0	543	4 AAB86206	Aab86206 Human hep
3	2841	100.0	543	7 ADD18950	Add18950 Human dis
4	2841	100.0	543	8 ADK52086	Adk52086 Human ato
5	2841	100.0	543	8 ADM48759	Adm48759 Human hpa
6	2841	100.0	543	8 ADN05074	Adn05074 Antipsori
7	2841	100.0	543	8 ADN04902	Adn04902 Antipsori
8	2841	100.0	543	8 ADQ80372	Adq80372 Heparanas
9	2841	100.0	543	8 ADR88210	Adr88210 Human pre
10	2841	100.0	543	8 ADP25079	Adp25079 PRO poly
11	2841	100.0	543	8 ADT78177	Adt78177 Human hep
12	2841	100.0	543	9 ADY27036	Ady27036 Human hep
13	2841	100.0	543	9 AEA42426	Aea42426 Human hep
14	2841	100.0	588	2 AAY30124	Aay30124 A human p
15	2838	99.9	543	2 AAY02345	Aay02345 A human h
16	2838	99.9	543	3 AAY57590	Aay57590 Human hep
17	2838	99.9	543	3 AAB08849	Aab08849 Amino aci
18	2838	99.9	543	3 AAB08849	Aab08849 Human hep
19	2838	99.9	543	4 AAY97635	Aay97635 Human hep
20	2838	99.9	543	5 ABB07813	Abb07813 Human hep
21	2838	99.9	543	7 ADG88800	Adg88800 Human hpa
22	2838	99.9	543	7 ADL16379	Adl16379 Human hep
23	2838	99.9	543	8 ADM48716	Adm48716 Human hpa
24	2838	99.9	543	9 AEA42466	Aea42466 Human hep

25	2838	99.9	592	2 AAY02346	Aay02346 A human h
26	2838	99.9	592	3 AAB08850	Aab08850 Amino aci
27	2838	99.9	592	7 ADG88804	Adg88804 Human SK-
28	2838	99.9	592	8 ADL16383	Adl16383 Human hep
29	2838	99.9	592	8 ADM48720	Adm48720 Human SK-
30	2838	99.9	592	9 AEA42461	Aea42461 Human hep
31	2835	99.8	543	8 ADO63831	Ado63831 Human hep
32	2835	99.8	543	8 ADO63823	Ado63823 Human hep
33	2835	99.8	543	8 ADO63832	Ado63832 Human hep
34	2835	99.8	543	8 ADO63822	Ado63822 Human hep
35	2829	99.6	543	4 AAB88361	Aab88361 Human mem
36	2829	99.6	543	8 ADO63824	Ado63824 Human hep
37	2829	99.6	543	9 ADY63087	Ady63087 Human clo
38	2824.5	99.4	556	9 ADZ19010	Adz19010 Heparanas
39	2820	99.3	545	6 ABP56822	Abp56822 Human hep
40	2820	99.3	545	7 ADE16012	Ade16012 G-coupled
41	2820	99.3	545	8 ADL93951	Adl93951 Human G-c
42	2807.5	98.8	570	9 ADZ19008	Adz19008 Heparanas
43	2767	97.4	530	2 AAY34173	Aay34173 Human pre
44	2740	96.4	532	2 AAY17083	Aay17083 Seq ID No
45	2695	94.9	527	9 ADZ19004	Adz19004 HepGS4 co

#### ALIGNMENTS

RESULT 1  
AAY17082  
ID AAY17082 standard; protein; 543 AA.  
XX AC AAY17082;  
XX DT 21-JUL-1999 (first entry)  
XX DE Human heparanase enzyme.  
XX KW Heparanase; endoglucuronidase; heparan sulfate proteoglycan; enzyme;  
KW metastasis; angiogenesis; wound healing; angioplasty-induced restenosis;  
KW arteriosclerosis; atherosclerosis; inflammation; tissue development;  
KW human; HSPG.  
XX OS Homo sapiens.  
XX FN WO9921975-A1.  
XX PD 06-MAY-1999.  
XX PF 28-OCT-1998; 98WO-AU000898.  
XX PR 28-OCT-1997; 97AU-00000062.  
XX PA 09-DEC-1997; 97AU-00000812.  
XX PI (AUSU) UNIV AUSTRALIAN NAT.  
XX DR Freeman CG, Hulet MD, Parish CR, Handorf BJ;  
DR WPI; 1999-312956/26.  
DR N-FSDB; AAX37259.  
XX PT Polynucleotides encoding mammalian endoglucuronidases, especially  
PT heparanases, useful to promote wound healing.  
XX PS Claim 6; Page 69-73; 112pp; English.  
XX CC The invention relates to nucleic acid sequences that encode heparanase  
CC enzymes having endoglucuronidase activity. Recombinant heparanases are  
CC capable of removing the HS side chain from heparan sulfate proteoglycan  
CC (HSPG). Sulfated oligosaccharides, sulphonates or HSPG can be used to  
CC inhibit heparanase, this is useful for treatment of a physiological or  
CC medical condition associated with elevated heparanase activity, such as  
CC metastasis, angiogenesis, wound healing, angioplasty-induced restenosis,  
CC arteriosclerosis, atherosclerosis and inflammation. The human, murine and  
CC rat heparanases can be used to enhance wound healing, especially

CC associated with tissue development and repair. The conditions mentioned  
CC above can be diagnosed using specific antibodies, and also using primers  
CC and probes specific for the heparanase polynucleotides. Other uses of the  
CC heparanases include sequencing sulfated molecules such as HSPG. The  
CC present sequence represents a human heparanase  
XX  
SQ Sequence 543 AA;

Query Match 100.0%; Score 2841; DB 2; Length 543;  
Best Local Similarity 100.0%; Pred. No. 3e-275;  
Matches 543; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLRSKPALPPMLLLGPGSPALPRPAQADVVLDLFTQEPHLHVPSPFLSVT 60  
DB 1 MLRSKPALPPMLLLGPGSPALPRPAQADVVLDLFTQEPHLHVPSPFLSVT 60

QY 61 IDANLATDPRFLILGSPKRLTLARGLSPAYLRFPGTKTDFLI FDPKKESTFEERSYMQS 120  
DB 61 IDANLATDPRFLILGSPKRLTLARGLSPAYLRFPGTKTDFLI FDPKKESTFEERSYMQS 120

QY 121 QVNQDICKYGSIPPDVEEKLREWPYQEQLLREHYQKFKNSTYRSRSDVLYTFANC 180  
DB 121 QVNQDICKYGSIPPDVEEKLREWPYQEQLLREHYQKFKNSTYRSRSDVLYTFANC 180

QY 181 GLDLIFGLNALLRTADLOWNSSNAQLLLDYCSSKGYNISWELGNPNPFLKKADIFINGS 240  
DB 181 GLDLIFGLNALLRTADLOWNSSNAQLLLDYCSSKGYNISWELGNPNPFLKKADIFINGS 240

QY 241 QLGEDFIQLHLLRSTFKNAKLYGPDVGQPRRTAKMLKSFLLKAGGEVIDSVTWHYYL 300  
DB 241 QLGEDFIQLHLLRSTFKNAKLYGPDVGQPRRTAKMLKSFLLKAGGEVIDSVTWHYYL 300

QY 301 NGRTATREDFLNPDVLDIFISSVQKVFQVVESTREPKKVMWLGTSAYGGAPLLSDTFA 360  
DB 301 NGRTATREDFLNPDVLDIFISSVQKVFQVVESTREPKKVMWLGTSAYGGAPLLSDTFA 360

QY 361 AGFMWLDKLGLSARMGIEVVMQVFFGAGNYHLVDENFDPLDYWLSLLFKLVGTVKVL 420  
DB 361 AGFMWLDKLGLSARMGIEVVMQVFFGAGNYHLVDENFDPLDYWLSLLFKLVGTVKVL 420

QY 421 ASVQGSKRRKRLRYLHCTNTDNPRYKEGDLTLAYINLHNVTKYRLPYPFNSKQVDKYLL 480  
DB 421 ASVQGSKRRKRLRYLHCTNTDNPRYKEGDLTLAYINLHNVTKYRLPYPFNSKQVDKYLL 480

QY 481 RPLGPHGLLSKSVQLNGLTLKMVDDOTLPLMEKPLRPGSSSLGLPAFSYFFVIRNAKVA 540  
DB 481 RPLGPHGLLSKSVQLNGLTLKMVDDOTLPLMEKPLRPGSSSLGLPAFSYFFVIRNAKVA 540

QY 541 ACT 543  
DB 541 ACT 543

RESULT 2  
AAB86206  
ID AAB86206 standard; protein; 543 AA.  
XX  
AC AAB86206;  
XX  
DT 24-AUG-2001 (first entry)  
XX  
DE Human heparanase inhibitor protein.  
XX  
KW Heparanase; inhibitor; cardiac insufficiency; cardiact; nephrotropic;  
KW hepatotropic; veterinary medicine; congestive heart failure; dyspnoea;  
KW primary cardiomyopathy; peripheral odema; pulmonary congestion;  
KW hepatic congestion; hydrothorax; ascite; nocturia; human.  
XX  
OS Homo sapiens.  
XX  
PN DE19955803-A1.  
XX  
PD 23-MAY-2001.

XX 19-NOV-1999; 99DE-01055803.  
PF 19-NOV-1999; 99DE-01055803.  
PR 19-NOV-1999; 99DE-01055803.  
XX (KNOL ) KNOLL AG.  
XX  
XX Herr D, Hahn A, Laux V;  
XX WPI; 2001-368371/39.  
DR N-PSDB; AAH20940.  
XX  
PT Treatment or prevention of cardiac insufficiency and related conditions,  
PT e.g. pulmonary congestion and dyspnoea, comprises administration of  
PT heparanase inhibitor.  
XX  
PS Disclosure; Page 11-13; 16pp; German.  
XX  
CC This invention describes a novel heparanase inhibitor which can be used  
CC for the treatment or prevention of cardiac insufficiency and associated  
CC indications, symptoms and/or malfunctions. The heparanase inhibitor of  
CC the invention has cardiant, nephrotropic and hepatotropic activity. The  
CC products of the invention can be used in human and veterinary medicine,  
CC for the treatment or prevention of congestive heart failure e.g. primary  
CC cardiomyopathy. Associated conditions treated or prevented with the  
CC inhibitor are especially peripheral odemas, pulmonary and hepatic  
CC congestion, dyspnoea, hydrothorax and ascites. Renal problems, e.g.  
CC nocturia, can also be treated. This sequence represents the human  
CC heparanase protein described in the method of the invention  
XX  
SQ Sequence 543 AA;

Query Match 100.0%; Score 2841; DB 4; Length 543;  
Best Local Similarity 100.0%; Pred. No. 3e-275;  
Matches 543; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLRSKPALPPMLLLGPGSPALPRPAQADVVLDLFTQEPHLHVPSPFLSVT 60  
DB 1 MLRSKPALPPMLLLGPGSPALPRPAQADVVLDLFTQEPHLHVPSPFLSVT 60

QY 61 IDANLATDPRFLILGSPKRLTLARGLSPAYLRFPGTKTDFLI FDPKKESTFEERSYMQS 120  
DB 61 IDANLATDPRFLILGSPKRLTLARGLSPAYLRFPGTKTDFLI FDPKKESTFEERSYMQS 120

QY 121 QVNQDICKYGSIPPDVEEKLREWPYQEQLLREHYQKFKNSTYRSRSDVLYTFANC 180  
DB 121 QVNQDICKYGSIPPDVEEKLREWPYQEQLLREHYQKFKNSTYRSRSDVLYTFANC 180

QY 181 GLDLIFGLNALLRTADLOWNSSNAQLLLDYCSSKGYNISWELGNPNPFLKKADIFINGS 240  
DB 181 GLDLIFGLNALLRTADLOWNSSNAQLLLDYCSSKGYNISWELGNPNPFLKKADIFINGS 240

QY 241 QLGEDFIQLHLLRSTFKNAKLYGPDVGQPRRTAKMLKSFLLKAGGEVIDSVTWHYYL 300  
DB 241 QLGEDFIQLHLLRSTFKNAKLYGPDVGQPRRTAKMLKSFLLKAGGEVIDSVTWHYYL 300

QY 301 NGRTATREDFLNPDVLDIFISSVQKVFQVVESTREPKKVMWLGTSAYGGAPLLSDTFA 360  
DB 301 NGRTATREDFLNPDVLDIFISSVQKVFQVVESTREPKKVMWLGTSAYGGAPLLSDTFA 360

QY 361 AGFMWLDKLGLSARMGIEVVMQVFFGAGNYHLVDENFDPLDYWLSLLFKLVGTVKVL 420  
DB 361 AGFMWLDKLGLSARMGIEVVMQVFFGAGNYHLVDENFDPLDYWLSLLFKLVGTVKVL 420

QY 421 ASVQGSKRRKRLRYLHCTNTDNPRYKEGDLTLAYINLHNVTKYRLPYPFNSKQVDKYLL 480  
DB 421 ASVQGSKRRKRLRYLHCTNTDNPRYKEGDLTLAYINLHNVTKYRLPYPFNSKQVDKYLL 480

QY 481 RPLGPHGLLSKSVQLNGLTLKMVDDOTLPLMEKPLRPGSSSLGLPAFSYFFVIRNAKVA 540  
DB 481 RPLGPHGLLSKSVQLNGLTLKMVDDOTLPLMEKPLRPGSSSLGLPAFSYFFVIRNAKVA 540

QY 541 ACT 543

```

Db      541 ACI 543

RESULT 3
ADD18950
ID ADD18950 standard; protein; 543 AA.
XX
AC ADD18950;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human disease related protein SeqID439.
XX
KW human; disease state; cytostatic; antiinflammatory; ophthalmological;
KW antiarteriosclerotic; vulnary; gene therapy;
KW hypoxia-regulated condition; tumorigenesis; angiogenesis; apoptosis;
KW inflammation; erythropoiesis; glycolysis; gluconeogenesis;
KW glucose transportation; catecholamine synthesis; iron transport;
KW nitric oxide synthesis; cancer; ischaemic condition; reperfusion injury;
KW retinopathy; neonatal stress; pre-eclampsia; atherosclerosis;
KW inflammatory condition; wound healing.
XX
OS Homo sapiens.
XX
FN WO2003018621-A2.
XX
PD 06-MAR-2003.
XX
PF 23-AUG-2002; 2002WO-GB003892.
XX
PR 23-AUG-2001; 2001GB-00020558.
XX
PR 05-OCT-2001; 2001GB-00024037.
XX
PA (OXFO-) OXFORD BIOMEDICA UK LTD.
XX
PI Kingsman SM, White J, Ward NR, Harris RA, Naylor S, Mundy CR;
XX
DR WPI; 2003-290046/28.
XX
DR N-PSDB; ADD18951.
XX
PT New substantially purified polypeptide, useful for diagnosing or treating
PT a hypoxia-regulated condition, such as cancer, ischemia, reperfusion
PT injury, retinopathy, pre-eclampsia, atherosclerosis, inflammation, or
PT wound healing.
XX
PS Claim 25; SEQ ID NO 439; 424pp; English.
XX
CC This invention relates to novel human genes and gene product which are
CC implicated in certain disease states. Compounds which modulate the
CC proteins of the invention may have cytostatic, antiinflammatory,
CC ophthalmological, antiarteriosclerotic or vulnerary activities. The
CC sequences of the invention may be useful for gene therapy. The invention
CC may be useful for diagnosing or treating a hypoxia-regulated condition,
CC such as tumorigenesis, angiogenesis, apoptosis, inflammation,
CC erythropoiesis, or the biological response to hypoxia conditions
CC including processes such as glycolysis, gluconeogenesis, glucose
CC transportation, catecholamine synthesis, iron transport or nitric oxide
CC synthesis. The disease includes cancer, ischaemic conditions, reperfusion
CC injury, retinopathy, neonatal stress, pre-eclampsia, atherosclerosis,
CC inflammatory conditions or wound healing. The present sequence is that of
CC a disease related protein of the invention.
XX
SQ Sequence 543 AA;

Query Match      100.0%; Score 2841; DB 7; Length 543;
Best Local Similarity 100.0%; Pred. No. 3e-275;
Matches 543; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 MLRSKALPPPLMLLLGLPLPGALPRPAQDVLDLDFETQPLHLVSPFLSVT 60
Db      1 MLRSKALPPPLMLLLGLPLPGALPRPAQDVLDLDFETQPLHLVSPFLSVT 60

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XX PS Example 2; SEQ ID NO 119; 484pp; Japanese.
XX CC The invention relates to detecting atopic dermatitis or psoriasis
CC comprising assaying the levels of expression of an indicator gene at a
CC rash site and non-rash site of a person with atopic dermatitis or
CC psoriasis, comparing these levels with those of a healthy person, and
CC determining that if the levels of indicators are higher or lower, then
CC this indicates the disease. Also included are a reagent for detecting
CC atopic dermatitis or psoriasis, a kit for screening for treatments, a
CC transgenic non human vertebrate animal models for the diseases, an agent
CC for inducing the diseases in mice and a DNA chip for assaying for the
CC indicator genes. The method is used for treatment, detection and animal
CC models for research of atopic dermatitis and psoriasis. The present
CC sequence is a protein encoded by an indicator gene of the invention.
XX SQ Sequence 543 AA;
    Query Match          100.0%; Score 2841; DB 8; Length 543;
    Best Local Similarity 100.0%; Pred. No. 3e-275;
    Matches 543; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLLRSKPALPPPLMLLLGLPLSPGALPRPAQAQDVVDLDFFTQEPHLHVSFSLSVT 60
Db 1 MLLRSKPALPPPLMLLLGLPLSPGALPRPAQAQDVVDLDFFTQEPHLHVSFSLSVT 60
QY 61 IDANLATDPRFLILGSPKRLTARGLSPAYLRFGGTKTDFLI FDPKKESTFEERSYWQS 120
Db 61 IDANLATDPRFLILGSPKRLTARGLSPAYLRFGGTKTDFLI FDPKKESTFEERSYWQS 120
QY 121 QVNQDICKYGSIPDPVEEKLRLWEPYQEQLLREHYQKFKNSTYSRSSVDVLYTFANCS 180
Db 121 QVNQDICKYGSIPDPVEEKLRLWEPYQEQLLREHYQKFKNSTYSRSSVDVLYTFANCS 180
QY 181 GLDLIFGLNALLRTADLQWSSNAQLLDYCSSKGYNISWELGNENPSFLKKADIFINGS 240
Db 181 GLDLIFGLNALLRTADLQWSSNAQLLDYCSSKGYNISWELGNENPSFLKKADIFINGS 240
QY 241 QLGEDFIQLHKLRLKSTFKNAKLYGPDVGPQRRTAKMLKSFLLKAGGEVIDSVTWHYYL 300
Db 241 QLGEDFIQLHKLRLKSTFKNAKLYGPDVGPQRRTAKMLKSFLLKAGGEVIDSVTWHYYL 300
QY 301 NGRTATREDFLNPDLVDIFISSQVKVFQVVESTPGKKVWLGETSAYGGAPLLSDTFA 360
Db 301 NGRTATREDFLNPDLVDIFISSQVKVFQVVESTPGKKVWLGETSAYGGAPLLSDTFA 360
QY 361 AGFMWLDKLGLSARMGIEVVMRQVFPAGNYHLVDENFDPLPDYWLILFKLVGTKVLM 420
Db 361 AGFMWLDKLGLSARMGIEVVMRQVFPAGNYHLVDENFDPLPDYWLILFKLVGTKVLM 420
QY 421 ASVQSGSKRRKRLRYLHCTNTDPRYKEGDLTLVAINLHNVTYLRPLPYPSNKKQVDKYL 480
Db 421 ASVQSGSKRRKRLRYLHCTNTDPRYKEGDLTLVAINLHNVTYLRPLPYPSNKKQVDKYL 480
QY 481 RPLGPHGLLSKSVQLNGLTLKWDDQTLPLPEMKPLRPGSSLGLPAPSYSFVIRNAKVA 540
Db 481 RPLGPHGLLSKSVQLNGLTLKWDDQTLPLPEMKPLRPGSSLGLPAPSYSFVIRNAKVA 540
QY 541 ACI 543
Db 541 ACI 543
RESULT 5
ADM48759 standard; protein; 543 AA.
XX ID ADM48759
XX AC ADM48759;
XX XX
DT 03-JUN-2004 (first entry)
XX DE Human hpa protein #2.
XX XX
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```
Transgenic animal; heparanase; cancer; viral infection; restenosis;
neurodegenerative disease; atherosclerosis; pulmonary disorder; hpa;
human.
XX OS Homo sapiens.
XX US2003217375-A1.
XX 20-NOV-2003.
XX 24-FEB-2003; 2003US-00371218.
XX 31-AUG-1998; 98WO-US017954.
XX 01-MAR-1999; 99US-00258892.
XX 06-FEB-2001; 2001US-00776874.
XX 19-NOV-2001; 2001US-00988113.
XX (ZCHA/) ZCHARIA E.
XX (VLDD/) VLDDAVSKY I.
XX (METZ/) METZGER S.
XX (PECK/) PECKER I.
XX (ILAN/) ILAN N.
XX (CHAJ/) CHAJEK-SHAUL T.
XX (GOLD/) GOLDSHMIDT O.
PI Zcharia E, Vloddavsky I, Metzger S, Pecker I, Ilan N;
PI Chajek-Shaul T, Goldshmidt O;
DR WPI; 2004-021918/02.
DR N-PSDB; ADM48748.
XX New transgenic non-human animal expressing heparinase, useful as models
XX for human disease, such as cancers, viral infection, neurodegenerative
XX diseases, restenosis, atherosclerosis and pulmonary disorders.
XX Example 10; Fig 16; 106pp; English.
XX The present invention relates to a transgenic non-human animal whose
XX genome comprises an exogenous polynucleotide sequence, including a
XX promoter active in tissues of the non-human, a region encoding a human
XX heparanase, where the promoter and the region encoding human heparanase
XX are operably linked in the exogenous polynucleotide such that human
XX heparanase is expressed in at least a portion of the cells of the non-
XX human animal. The methods and compositions of the present invention are
XX useful for the production of transgenic animals expressing heparanase, to
XX be used as models for human diseases such as cancers, viral infection,
XX restenosis, neurodegenerative diseases, atherosclerosis and pulmonary
XX disorders. The present sequence is human hpa protein used in the
XX exemplification of the invention.
XX SQ Sequence 543 AA;
    Query Match          100.0%; Score 2841; DB 8; Length 543;
    Best Local Similarity 100.0%; Pred. No. 3e-275;
    Matches 543; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLLRSKPALPPPLMLLLGLPLSPGALPRPAQAQDVVDLDFFTQEPHLHVSFSLSVT 60
Db 1 MLLRSKPALPPPLMLLLGLPLSPGALPRPAQAQDVVDLDFFTQEPHLHVSFSLSVT 60
QY 61 IDANLATDPRFLILGSPKRLTARGLSPAYLRFGGTKTDFLI FDPKKESTFEERSYWQS 120
Db 61 IDANLATDPRFLILGSPKRLTARGLSPAYLRFGGTKTDFLI FDPKKESTFEERSYWQS 120
QY 121 QVNQDICKYGSIPDPVEEKLRLWEPYQEQLLREHYQKFKNSTYSRSSVDVLYTFANCS 180
Db 121 QVNQDICKYGSIPDPVEEKLRLWEPYQEQLLREHYQKFKNSTYSRSSVDVLYTFANCS 180
QY 181 GLDLIFGLNALLRTADLQWSSNAQLLDYCSSKGYNISWELGNENPSFLKKADIFINGS 240
Db 181 GLDLIFGLNALLRTADLQWSSNAQLLDYCSSKGYNISWELGNENPSFLKKADIFINGS 240
QY 241 QLGEDFIQLHKLRLKSTFKNAKLYGPDVGPQRRTAKMLKSFLLKAGGEVIDSVTWHYYL 300
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Db      241  QLGEDFIQLHLKLRKSTFKNAKLYGPDVGQPRRTAKMLKSFLLKAGGEVIDSVTWHYYL 300
QY      301  NGRTATREDFLNPDVLDIFISSVQKVFQVVESTRPGKVKVWLGETSSAYGGGAPLLSDTFA 360
Db      301  NGRTATREDFLNPDVLDIFISSVQKVFQVVESTRPGKVKVWLGETSSAYGGGAPLLSDTFA 360
QY      361  AGFMWLDKGLSARMGIEVVMRQVFFGAGNYHLVDENFDPLPDYWLSSLFKKLVGTVKVL 420
Db      361  AGFMWLDKGLSARMGIEVVMRQVFFGAGNYHLVDENFDPLPDYWLSSLFKKLVGTVKVL 420
QY      421  ASVQSKRRKLRVYLHCTNTDPRYKEGDLTLIAINLHNVTYKYLRLPYFNSKQVDKYL 480
Db      421  ASVQSKRRKLRVYLHCTNTDPRYKEGDLTLIAINLHNVTYKYLRLPYFNSKQVDKYL 480
QY      481  RPLGPHGLLSKSVQNLGLTLKMVDDQTLPLMEKPLRPGSSLGLPAPFSYSPFVIRNAKVA 540
Db      481  RPLGPHGLLSKSVQNLGLTLKMVDDQTLPLMEKPLRPGSSLGLPAPFSYSPFVIRNAKVA 540
QY      541  ACI 543
Db      541  ACI 543

```

## RESULT 6

```

ADN05074
ID      ADN05074 standard; protein; 543 AA.
XX
AC      ADN05074;
XX
DT      01-JUL-2004 (first entry)
XX
DE      Antipsoriatic protein sequence #716.
XX
KW      antipsoriatic; gene therapy; psoriasis; diagnosis.
XX
OS      Homo sapiens.
XX
FN      WO2004028479-A2.
XX
PD      08-APR-2004.
XX
PF      25-SEP-2003; 2003WO-US030907.
XX
PR      25-SEP-2002; 2002US-0414006P.
XX
PA      (GETH ) GENENTECH INC.
XX
PI      Bodary S, Clark H, Jackman J, Schoenfeld J, Williams PM, Wood WI;
PI      Wu TD;
XX
DR      WPI; 2004-305105/28.
XX
DR      N-PSDB; ADN05073.
XX
FT      New PRO nucleic acid or polypeptide, useful for preparing a
FT      pharmaceutical composition for diagnosing or treating psoriasis in a
FT      mammal.
XX
PS      Claim 9; SEQ ID NO 1468; 3069pp; English.
XX
CC      The invention relates to novel polynucleotide and polypeptides for
CC      treating psoriasis or a sequence having at least 80% identity to the
CC      above sequences. The nucleic acid is useful for preparing a composition
CC      for diagnosing or treating psoriasis in a mammal. This sequence
CC      corresponds to one of the polypeptides of the invention.
XX
SQ      Sequence 543 AA;

```

```

Query Match      100.0%; Score 2841; DB 8; Length 543;
Best Local Similarity 100.0%; Pred. No. 3e-275;
Matches 543; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

QY      1  MLLRSKPALPPPLMLLLGLPLSPGALPRPAQADVVLDLFFFTQEPHLVSPSFLSVT 60

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Db      1  MLLRSKPALPPPLMLLLGLPLSPGALPRPAQADVVLDLFFFTQEPHLVSPSFLSVT 60
QY      61  IDANLATDPRFLILGLSPKRLTARGLSPAYLRFGGTKTDFLI FPKKKESTFEERSYWS 120
Db      61  IDANLATDPRFLILGLSPKRLTARGLSPAYLRFGGTKTDFLI FPKKKESTFEERSYWS 120
QY      121  QVNQDICKYGSIPPDVEEKLRLWPYQQLLLREHYQKKFNKNSTYSRSSVDVLYTFANCS 180
Db      121  QVNQDICKYGSIPPDVEEKLRLWPYQQLLLREHYQKKFNKNSTYSRSSVDVLYTFANCS 180
QY      181  GLDLIFGLNALLRTADLQWNSNAQLLLDYCSSKGYNISWELGNBPNSFLKKADIFINGS 240
Db      181  GLDLIFGLNALLRTADLQWNSNAQLLLDYCSSKGYNISWELGNBPNSFLKKADIFINGS 240
QY      241  QLGEDFIQLHLKLRKSTFKNAKLYGPDVGQPRRTAKMLKSFLLKAGGEVIDSVTWHYYL 300
Db      241  QLGEDFIQLHLKLRKSTFKNAKLYGPDVGQPRRTAKMLKSFLLKAGGEVIDSVTWHYYL 300
QY      301  NGRTATREDFLNPDVLDIFISSVQKVFQVVESTRPGKVKVWLGETSSAYGGGAPLLSDTFA 360
Db      301  NGRTATREDFLNPDVLDIFISSVQKVFQVVESTRPGKVKVWLGETSSAYGGGAPLLSDTFA 360
QY      361  AGFMWLDKGLSARMGIEVVMRQVFFGAGNYHLVDENFDPLPDYWLSSLFKKLVGTVKVL 420
Db      361  AGFMWLDKGLSARMGIEVVMRQVFFGAGNYHLVDENFDPLPDYWLSSLFKKLVGTVKVL 420
QY      421  ASVQSKRRKLRVYLHCTNTDPRYKEGDLTLIAINLHNVTYKYLRLPYFNSKQVDKYL 480
Db      421  ASVQSKRRKLRVYLHCTNTDPRYKEGDLTLIAINLHNVTYKYLRLPYFNSKQVDKYL 480
QY      481  RPLGPHGLLSKSVQNLGLTLKMVDDQTLPLMEKPLRPGSSLGLPAPFSYSPFVIRNAKVA 540
Db      481  RPLGPHGLLSKSVQNLGLTLKMVDDQTLPLMEKPLRPGSSLGLPAPFSYSPFVIRNAKVA 540
QY      541  ACI 543
Db      541  ACI 543

```

## RESULT 7

```

ADN04902
ID      ADN04902 standard; protein; 543 AA.
XX
AC      ADN04902;
XX
DT      01-JUL-2004 (first entry)
XX
DE      Antipsoriatic protein sequence #631.
XX
KW      antipsoriatic; gene therapy; psoriasis; diagnosis.
XX
OS      Homo sapiens.
XX
FN      WO2004028479-A2.
XX
PD      08-APR-2004.
XX
PF      25-SEP-2003; 2003WO-US030907.
XX
PR      25-SEP-2002; 2002US-0414006P.
XX
PA      (GETH ) GENENTECH INC.
XX
PI      Bodary S, Clark H, Jackman J, Schoenfeld J, Williams PM, Wood WI;
PI      Wu TD;
XX
DR      WPI; 2004-305105/28.
DR      N-PSDB; ADN04901.
XX
FT      New PRO nucleic acid or polypeptide, useful for preparing a
FT      pharmaceutical composition for diagnosing or treating psoriasis in a
FT      mammal.

```

```
XX PS Claim 9; SEQ ID NO 1296; 3069pp; English.
XX CC
XX CC The invention relates to novel polynucleotide and polypeptides for
XX CC treating psoriasis or a sequence having at least 80% identity to the
XX CC above sequences. The nucleic acid is useful for preparing a composition
XX CC for diagnosing or treating psoriasis in a mammal. This sequence
XX CC corresponds to one of the polypeptides of the invention.
XX SQ Sequence 543 AA;

Query Match 100.0%; Score 2841; DB 8; Length 543;
Best Local Similarity 100.0%; Pred. No. 3e-275;
Matches 543; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLRSKPALPPPLMLLLGPGPLSPGALPRPAQAQDVVDLDFFTQEPHLHVSFSLVY 60
Db 1 MLRSKPALPPPLMLLLGPGPLSPGALPRPAQAQDVVDLDFFTQEPHLHVSFSLVY 60

Qy 61 IDANLATDPRFLLILGSPKRLTLARGLSPAYLRFSGTKTDFLIDPKKESTFEERSYQWS 120
Db 61 IDANLATDPRFLLILGSPKRLTLARGLSPAYLRFSGTKTDFLIDPKKESTFEERSYQWS 120

Qy 121 QVNQDICKYGSIPDPVEEKLRLWPYQEQOLLREHYQKFKNSTYRSRSDVLYTFANCS 180
Db 121 QVNQDICKYGSIPDPVEEKLRLWPYQEQOLLREHYQKFKNSTYRSRSDVLYTFANCS 180

Qy 181 GJDLIFGLNALLRTADLQWNSNAQLLDYCSSKGYNISWELGNEPNSFLKKADIFINGS 240
Db 181 GJDLIFGLNALLRTADLQWNSNAQLLDYCSSKGYNISWELGNEPNSFLKKADIFINGS 240

Qy 241 QLGEDFIQLHKLRLKSTFNKALYGPVQGPQRRTAKMLKSLFKAGGEVIDSVTHHHYL 300
Db 241 QLGEDFIQLHKLRLKSTFNKALYGPVQGPQRRTAKMLKSLFKAGGEVIDSVTHHHYL 300

Qy 301 NGRTATREDFLNPDVLDIFISSVQKVFQVVESTPGKKVWLGETSSAYGGAPLLSDTFA 360
Db 301 NGRTATREDFLNPDVLDIFISSVQKVFQVVESTPGKKVWLGETSSAYGGAPLLSDTFA 360

Qy 361 AGFMWLDKLGSLARMGIEVVMQVFFGAGNYHLVDENFDPLPDYWLSSLFVKLVGTVKVL 420
Db 361 AGFMWLDKLGSLARMGIEVVMQVFFGAGNYHLVDENFDPLPDYWLSSLFVKLVGTVKVL 420

Qy 421 ASVQSGKRRKRLRVYLHCTNTDNPYKEGDLTLVAINLHNVTKYLRPLPYFSPNKQVDKYL 480
Db 421 ASVQSGKRRKRLRVYLHCTNTDNPYKEGDLTLVAINLHNVTKYLRPLPYFSPNKQVDKYL 480

Qy 541 ACI 543
Db 541 ACI 543

RESULT 8
ADQ80372
ID ADQ80372 standard; protein; 543 AA.
XX AC
XX AC ADQ80372;
XX DT
XX DT 21-OCT-2004 (first entry)
XX DE Heparanase protein.
XX XX
XX KW cytostatic; epidermal growth factor receptor modulator; identification;
XX KW therapeutic response; cancer; EGFR; biomarker.
XX OS Homo sapiens.
XX PN WO2004063709-A2.
XX XX
```

```
PD 29-JUL-2004.
XX XX
XX PF 08-JAN-2004; 2004WO-US000368.
XX XX
XX PR 08-JAN-2003; 2003US-0438735P.
XX XX
XX PA (BRIM ) BRISTOL-MYERS SQUIBB CO.
XX XX
XX PI Amler LC, Januario T;
XX XX
XX DR WPI; 2004-544114/52.
XX DR N-PSDB; ADQ80253.
XX XX
XX PT Identifying a mammal that will respond therapeutically to a method of
XX PT treating cancer comprises comparing the level of a biomarker in a mammal
XX PT before and after exposure to an epidermal growth factor receptor (EGFR)
XX PT modulator.
XX XX
XX PS Disclosure; SEQ ID NO 144; 520pp; English.
XX XX
XX CC The invention relates to a method of identifying a mammal that will
XX CC respond therapeutically to a method of treating cancer by administering
XX CC an epidermal growth factor receptor (EGFR) modulator by comparing the
XX CC level of a biomarker in a mammal before and after exposure to an EGFR
XX CC modulator. The method comprises: (a) measuring, in the mammal, the level
XX CC of at least one biomarker identified in the specification; (b) exposing
XX CC the mammal to the EGFR modulator; and (c) measuring in the mammal the
XX CC level of the biomarker, where a difference in the level in step (c)
XX CC compared to step (a) indicates that the mammal will respond
XX CC therapeutically to the method of treating cancer. The method and
XX CC biomarkers are useful for identifying a mammal that will respond
XX CC therapeutically to a method of treating cancer by administering an
XX CC epidermal growth factor receptor (EGFR) modulator. This sequence
XX CC corresponds to one of the biomarkers whose levels of expression is
XX CC measured in the method of the invention.
XX SQ Sequence 543 AA;

Query Match 100.0%; Score 2841; DB 8; Length 543;
Best Local Similarity 100.0%; Pred. No. 3e-275;
Matches 543; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLRSKPALPPPLMLLLGPGPLSPGALPRPAQAQDVVDLDFFTQEPHLHVSFSLVY 60
Db 1 MLRSKPALPPPLMLLLGPGPLSPGALPRPAQAQDVVDLDFFTQEPHLHVSFSLVY 60

Qy 61 IDANLATDPRFLLILGSPKRLTLARGLSPAYLRFSGTKTDFLIDPKKESTFEERSYQWS 120
Db 61 IDANLATDPRFLLILGSPKRLTLARGLSPAYLRFSGTKTDFLIDPKKESTFEERSYQWS 120

Qy 121 QVNQDICKYGSIPDPVEEKLRLWPYQEQOLLREHYQKFKNSTYRSRSDVLYTFANCS 180
Db 121 QVNQDICKYGSIPDPVEEKLRLWPYQEQOLLREHYQKFKNSTYRSRSDVLYTFANCS 180

Qy 181 GJDLIFGLNALLRTADLQWNSNAQLLDYCSSKGYNISWELGNEPNSFLKKADIFINGS 240
Db 181 GJDLIFGLNALLRTADLQWNSNAQLLDYCSSKGYNISWELGNEPNSFLKKADIFINGS 240

Qy 241 QLGEDFIQLHKLRLKSTFNKALYGPVQGPQRRTAKMLKSLFKAGGEVIDSVTHHHYL 300
Db 241 QLGEDFIQLHKLRLKSTFNKALYGPVQGPQRRTAKMLKSLFKAGGEVIDSVTHHHYL 300

Qy 301 NGRTATREDFLNPDVLDIFISSVQKVFQVVESTPGKKVWLGETSSAYGGAPLLSDTFA 360
Db 301 NGRTATREDFLNPDVLDIFISSVQKVFQVVESTPGKKVWLGETSSAYGGAPLLSDTFA 360

Qy 361 AGFMWLDKLGSLARMGIEVVMQVFFGAGNYHLVDENFDPLPDYWLSSLFVKLVGTVKVL 420
Db 361 AGFMWLDKLGSLARMGIEVVMQVFFGAGNYHLVDENFDPLPDYWLSSLFVKLVGTVKVL 420

Qy 421 ASVQSGKRRKRLRVYLHCTNTDNPYKEGDLTLVAINLHNVTKYLRPLPYFSPNKQVDKYL 480
Db 421 ASVQSGKRRKRLRVYLHCTNTDNPYKEGDLTLVAINLHNVTKYLRPLPYFSPNKQVDKYL 480
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QY 481 RPLGPHGLSKSVQLNGLTKMVDQDTLPPLMEKPLRPGSSLGLPFAFSYSPFVIRNAKVA 540
Db 481 RPLGPHGLSKSVQLNGLTKMVDQDTLPPLMEKPLRPGSSLGLPFAFSYSPFVIRNAKVA 540
QY 541 ACI 543
Db 541 ACI 543

RESULT 9
ID ADR88210 standard; protein; 543 AA.
AC ADR88210;
XX
DT 18-NOV-2004 (first entry)
XX
DE Human preproheparanase.
XX
KW Targeted drug delivery; inflammatory disorder; wound; scar; vasculopathy;
KW autoimmune disorder; cancer; angiogenesis; metastatic disease;
KW atherosclerosis; restenosis; aneurysm; solid cancer; non-solid cancer;
KW haematopoietic malignancy; lymphocytic leukaemia; myelogenous leukaemia;
KW Hodgkin's disease; multiple myeloma; haemangiosarcoma; Kaposi's sarcoma;
KW human; heparanase; enzyme.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..35
FT Protein /label= Signal_peptide
FT Region /label= Mature_heparanase
FT Domain /note= "8 KDa subunit of mature heparanase dimer"
FT Region /note= "Functional peptide epitope"
FT Domain /note= "45 KDa subunit of mature heparanase dimer"
FT Active-site /note= "Functional peptide epitope"
FT Binding-site /note= "Active site residue"
FT Domain /note= "Putative heparin binding domain"
FT Domain /note= "Functional peptide epitope"
FT Domain /note= "Functional peptide epitope"
FT Active-site /note= "Active site residue"
FT Binding-site /note= "Putative heparin binding domain"
FT Domain /note= "Functional peptide epitope"

US2004170631-A1.
02-SEP-2004.
28-NOV-2003; 2003US-00722502.
02-SEP-1997; 97US-00922170.
01-MAY-1998; 98US-00071739.
04-NOV-1998; 98US-00186200.
19-FEB-2003; 2003US-00368044.
22-AUG-2003; 2003US-00645659.
(YACO/) YACOBY-ZEEVI O.
(PERE/) PERETZ T.
(MIRO/) MIRON D.
(SHLO/) SHLOMI Y.

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PA (PECK/) PECKER I.
PA (AYAL/) AYAL-HERSHKOVITZ M.
PA (FEIN/) FEINSTEIN E.
PA (VCEL/) VAN GELDER J M.
PA (VLOD/) VLODAVSKY I.
PA (FRIE/) FRIEDMANN Y.
PI Yacoby-Zeevi O, Peretz T, Miron D, Shlomi Y, Pecker I;
PI Ayal-HersHKovitz M, Feinstein E, Van Gelder JM, Vlodavsky I;
PI Friedmann Y;
XX WPI; 2004-625084/60.
DR
XX
PT Targeted drug delivery to a heparanase-expressing tissue of a patient,
PT useful for treating heparanase-associated conditions such as inflammation
PT or cancer, comprises administering a drug and an anti-heparanase antibody
PT complex.
XX
PS Claim 2; SEQ ID NO 4; 58pp; English.
XX
CC The invention relates to a method of targeted drug delivery to a tissue
CC of a patient, the tissue expressing heparanase. The method comprises
CC providing a complex of a drug directly or indirectly linked to an anti-
CC heparanase antibody, and administering the complex to the patient. In the
CC targeted drug delivery, the antibody comprises an antibody or its portion
CC capable of specifically binding to at least one epitope of a heparanase
CC protein. The composition and methods of the invention are useful for
CC diagnosing, preventing or treating conditions associated with heparanase
CC catalytic activity (e.g. an inflammatory disorder, wound, scar,
CC vasculopathy, an autoimmune disorder, cancer, angiogenesis, cell
CC proliferation, invasion of circulating tumour cells and metastatic
CC disease), for purifying heparanase, or for developing drugs for those
CC heparanase-associated conditions. The vasculopathy is atherosclerosis,
CC restenosis or aneurysm. The cancerous condition is a solid cancer or a
CC non-solid cancer. The non-solid cancer is a haematopoietic malignancy
CC selected from acute lymphocytic leukaemia (ALL), acute myelogenous
CC leukaemia, chronic lymphocytic leukaemia (CLL), chronic myelogenous
CC leukaemia (CML), myelodysplastic syndrome (MDS), mast cell leukaemia,
CC Hodgkin's disease, non-Hodgkin's lymphomas, Burkitt's lymphoma and
CC multiple myeloma. The solid cancer is selected from tumours in lip and
CC oral cavity, pharynx, larynx, paranasal sinuses, major salivary glands,
CC thyroid gland, oesophagus, stomach, small intestine, colon, colorectum,
CC anal canal, liver, gallbladder, extrahepatic bile ducts, ampulla of
CC Vater, exocrine pancreas, lung, pleural mesothelioma, soft tissue
CC sarcoma, carcinoma and malignant melanoma of the skin, breast, vulva,
CC vagina, cervix uteri, ovary, fallopian tube, gestational trophoblastic
CC tumours, penis, prostate, testis, kidney, renal pelvis, ureter, urinary
CC bladder, urethra, carcinoma of the eyelid, carcinoma of the conjunctiva,
CC malignant melanoma of the conjunctiva, malignant melanoma of the uvea,
CC retinoblastoma, carcinoma of the lacrimal gland, sarcoma of the orbit,
CC brain, spinal cord, vascular system, haemangiosarcoma and Kaposi's
CC sarcoma. The present sequence is human preproheparanase.
XX
SQ Sequence 543 AA;
Query Match 100.0%; Score 2841; DB 8; Length 543;
Best Local Similarity 100.0%; Pred. No. 3e-275;
Matches 543; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MLRSKPALPPPLMLLLGLPLSPGALPRPAQDVVDLDFFTQBPFLHVLVSFSLSVT 60
Db 1 MLRSKPALPPPLMLLLGLPLSPGALPRPAQDVVDLDFFTQBPFLHVLVSFSLSVT 60
Qy 61 IDANLATDPRFLILGSPKLTARGLSPAYLRGGTKTDLIDPKKESFEERSYQWS 120
Db 61 IDANLATDPRFLILGSPKLTARGLSPAYLRGGTKTDLIDPKKESFEERSYQWS 120
Qy 121 QVNQDICKYGSIPDPVEEKLREWPYQEQLLRREHYOKFKNKYSTYSSVDVLYTFANCS 180
Db 121 QVNQDICKYGSIPDPVEEKLREWPYQEQLLRREHYOKFKNKYSTYSSVDVLYTFANCS 180
Qy 181 GLDLIFGLNALLRTADLQWNSSNAQLLDYCSCSGYNISWELGNPNPSFLKADIFINGS 240
Db 181 GLDLIFGLNALLRTADLQWNSSNAQLLDYCSCSGYNISWELGNPNPSFLKADIFINGS 240

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Db 181 GLDLIFGLNALLRTADLQWSSNAQLLLDYCSSKGYNISWELGNPNFLKKADIFINGS 240  
 QY 241 QLGEDFIQLHKLRLKSTFKNAKLYGPDVGVQPRKRTAKMLKSLFKAGGVEIDSVTWHYYL 300  
 Db 241 QLGEDFIQLHKLRLKSTFKNAKLYGPDVGVQPRKRTAKMLKSLFKAGGVEIDSVTWHYYL 300  
 QY 301 NGRTATREDFLNPDVLDIFISSVQKVFQVVESTRGKKVWLGETSSAYGGAPLLSDTFA 360  
 Db 301 NGRTATREDFLNPDVLDIFISSVQKVFQVVESTRGKKVWLGETSSAYGGAPLLSDTFA 360  
 QY 361 AGFMWLDKGLSARMGIEVVMQVFFGAGNYHLVDENFDPLPDYWLSSLFKKLVGTVKVL 420  
 Db 361 AGFMWLDKGLSARMGIEVVMQVFFGAGNYHLVDENFDPLPDYWLSSLFKKLVGTVKVL 420  
 QY 421 ASVQGSKRRKRLRVYLHCTNTDNPRYKEGDLTIYALNHNVTYKLRPLPYFSPSNKQVDKYL 480  
 Db 421 ASVQGSKRRKRLRVYLHCTNTDNPRYKEGDLTIYALNHNVTYKLRPLPYFSPSNKQVDKYL 480  
 QY 481 RPLGPHGLLSKSVQLNGLTLKMWDDQTLPLMEKPLRPGSSSLGLPAFSYSFFVIRNAKVA 540  
 Db 481 RPLGPHGLLSKSVQLNGLTLKMWDDQTLPLMEKPLRPGSSSLGLPAFSYSFFVIRNAKVA 540  
 QY 541 ACI 543  
 Db 541 ACI 543  
 RESULT 10  
 ADP25079  
 ID ADP25079 standard; protein; 543 AA.  
 XX  
 AC ADP25079;  
 DT 18-NOV-2004 (first entry)  
 XX  
 DE PRO polypeptide SEQ ID NO:2257.  
 KW PRO; antiinflammatory; antiarthritic; antirheumatic; immunosuppressive;  
 KW osteopathic; antidiabetic; dermatological; antipsoriatic; antiallergic;  
 KW antiasthmatic; hepatotropic; respiratory; gene therapy; immune system.  
 XX  
 OS Unidentified.  
 XX  
 FN WO2004041170-A2.  
 XX  
 PD 21-MAY-2004.  
 XX  
 PF 30-OCT-2003; 2003WO-US034312.  
 XX  
 PR 01-NOV-2002; 2002US-0423394P.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX  
 PI Clark H, Schoenfeld J, Van Lookeren M, Williams PM, Wood WI;  
 PI Wu TD;  
 XX  
 DR WPI; 2004-419628/39.  
 XX  
 DR N-PSDB; ADP25078.  
 XX  
 XX New PRO polypeptides and polynucleotides, useful for treating e.g.  
 PT erythematous, rheumatoid arthritis, diabetes mellitus, immune-mediated  
 PT renal disease, or demyelinating diseases of the central or peripheral  
 PT nervous system.  
 XX  
 XX Claim 7; SEQ ID NO 2257; 2940pp; English.  
 PS  
 XX The invention relates to a novel isolated nucleic acid and the PRO  
 CC polypeptide encoded by it. A protein of the invention has  
 CC antiinflammatory, antirheumatic, antirheumatic, immunosuppressive,  
 CC osteopathic, antidiabetic, dermatological, antipsoriatic, antiallergic,  
 CC antiasthmatic, hepatotropic, and respiratory activity. A polynucleotide  
 CC of the invention may have a use in gene therapy. The PRO polypeptide, its  
 CC agonist, antagonist, or antibody that specifically binds to the

CC polypeptide is useful for treating an immune related disorder such as  
 CC systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,  
 CC juvenile chronic arthritis, a spondyloarthropathy, systemic sclerosis, an  
 CC idiopathic inflammatory myopathy, Sjogren's syndrome, systemic  
 CC vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune  
 CC thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal  
 CC disease, a demyelinating disease of the central or peripheral nervous  
 CC system, idiopathic demyelinating polyneuropathy, Guillain-Barre syndrome,  
 CC a chronic inflammatory demyelinating polyneuropathy, a hepatobiliary  
 CC disease, infectious or autoimmune chronic active hepatitis, primary  
 CC biliary cirrhosis, granulomatous hepatitis, sclerosing cholangitis,  
 CC inflammatory bowel disease, gluten-sensitive enteropathy, Whipple's  
 CC disease, an autoimmune or immune-mediated skin disease, a bullous skin  
 CC disease, erythema multiforme, contact dermatitis, psoriasis, an allergic  
 CC disease, asthma, allergic rhinitis, atopic dermatitis, food  
 CC hypersensitivity, urticaria, an immunologic disease of the lung,  
 CC eosinophilic pneumonia, idiopathic pulmonary fibrosis, hypersensitivity  
 CC pneumonitis, a transplantation associated disease, graft rejection or  
 CC graft-versus-host disease. The present sequence represents a PRO protein  
 CC of the invention.  
 XX  
 SQ Sequence 543 AA;  
 Query Match 100.0%; Score 2841; DB 8; Length 543;  
 Best Local Similarity 100.0%; Pred. No. 3e-275;  
 Matches 543; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MLRSKPALPPPLMLLLGLPLSPGALPRPAQADVVLDLDFQTEPLHLVSPSFLSVT 60  
 Db 1 MLRSKPALPPPLMLLLGLPLSPGALPRPAQADVVLDLDFQTEPLHLVSPSFLSVT 60  
 QY 61 IDANLATDPRFLIILGSPKRLTLARGLSPAYLRFQGTGTDLIIDPKKESFEESYMQS 120  
 Db 61 IDANLATDPRFLIILGSPKRLTLARGLSPAYLRFQGTGTDLIIDPKKESFEESYMQS 120  
 QY 121 QVNQDICKYGSIPDPVEEKLRLWPYQQLLREHYQKFKNSTYSRSSVDVLYTFANC 180  
 Db 121 QVNQDICKYGSIPDPVEEKLRLWPYQQLLREHYQKFKNSTYSRSSVDVLYTFANC 180  
 QY 181 GLDLIFGLNALLRTADLQWSSNAQLLLDYCSSKGYNISWELGNPNFLKKADIFINGS 240  
 Db 181 GLDLIFGLNALLRTADLQWSSNAQLLLDYCSSKGYNISWELGNPNFLKKADIFINGS 240  
 QY 241 QLGEDFIQLHKLRLKSTFKNAKLYGPDVGVQPRKRTAKMLKSLFKAGGVEIDSVTWHYYL 300  
 Db 241 QLGEDFIQLHKLRLKSTFKNAKLYGPDVGVQPRKRTAKMLKSLFKAGGVEIDSVTWHYYL 300  
 QY 301 NGRTATREDFLNPDVLDIFISSVQKVFQVVESTRGKKVWLGETSSAYGGAPLLSDTFA 360  
 Db 301 NGRTATREDFLNPDVLDIFISSVQKVFQVVESTRGKKVWLGETSSAYGGAPLLSDTFA 360  
 QY 361 AGFMWLDKGLSARMGIEVVMQVFFGAGNYHLVDENFDPLPDYWLSSLFKKLVGTVKVL 420  
 Db 361 AGFMWLDKGLSARMGIEVVMQVFFGAGNYHLVDENFDPLPDYWLSSLFKKLVGTVKVL 420  
 QY 421 ASVQGSKRRKRLRVYLHCTNTDNPRYKEGDLTIYALNHNVTYKLRPLPYFSPSNKQVDKYL 480  
 Db 421 ASVQGSKRRKRLRVYLHCTNTDNPRYKEGDLTIYALNHNVTYKLRPLPYFSPSNKQVDKYL 480  
 QY 481 RPLGPHGLLSKSVQLNGLTLKMWDDQTLPLMEKPLRPGSSSLGLPAFSYSFFVIRNAKVA 540  
 Db 481 RPLGPHGLLSKSVQLNGLTLKMWDDQTLPLMEKPLRPGSSSLGLPAFSYSFFVIRNAKVA 540  
 QY 541 ACI 543  
 Db 541 ACI 543  
 RESULT 11  
 ADT78177  
 ID ADT78177 standard; protein; 543 AA.  
 XX  
 XX ADT78177;  
 AC

XX 13-JAN-2005 (first entry)  
 XX Human heparanase protein.  
 XX  
 KW Antibody; epitope; heparanase; pathological condition; angiogenesis;  
 KW cell proliferation; cancerous condition; tumour cell invasion;  
 KW metastatic disease; heparanase-related disorder; inflammatory disorder;  
 KW wound; scar; vasculopathy; autoimmune condition; renal disease;  
 KW cytostatic; antiinflammatory; vulnery; antiarteriosclerotic;  
 KW vasotropic; immunosuppressive; nephrotropic; antidiabetic; human.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key  
 FT Binding-site 157..162 Location/Qualifiers  
 FT /note= "Putative heparin binding site"  
 FT Binding-site 271..277  
 FT /note= "Putative heparin binding site"  
 FT Binding-site 426..433  
 FT /note= "Putative heparin binding site"  
 XX  
 US2004213789-A1.  
 XX  
 XX 28-OCT-2004.  
 PD  
 XX  
 XX 22-AUG-2003; 2003US-00645659.  
 XX  
 XX 02-SEP-1997; 97US-00922170.  
 PR  
 XX 01-MAY-1998; 98US-00071739.  
 PR  
 XX 04-NOV-1998; 98US-00186200.  
 PR  
 XX 19-FEB-2003; 2003US-00368044.  
 PR  
 XX  
 PA (YACO/) YACOBY-ZEEVI O.  
 PA (PERE/) PERETZ T.  
 PA (MIRO/) MIRON D.  
 PA (SHLO/) SHLOMI Y.  
 PA (PECK/) PECKER I.  
 PA (AYAL/) AYAL-HERSHKOVITZ M.  
 PA (FEIN/) FEINSTEIN E.  
 PA (GELD/) GELDER J M V.  
 PA (VLOD/) VLODAVSKY I.  
 PA (FRIE/) FRIEDMANN Y.  
 XX  
 XX Yacoby-Zeevi O, Peretz T, Miron D, Shlomi Y, Pecker I;  
 PI Ayal-Herskovitz M, Feinstein E, Gelder JMW, Vlodavsky I;  
 PI Friedmann Y;  
 XX  
 XX WPI; 2004-774790/76.  
 DR  
 XX  
 XX New neutralizing monoclonal anti-heparanase antibodies, useful for  
 FT detecting, treating or preventing cancer, inflammatory or autoimmune  
 FT disorder, wound, atherosclerosis, restenosis, or diabetic nephropathy.  
 PT  
 XX  
 FS Claim 5; SEQ ID NO 4; 68pp; English.  
 XX  
 XX The invention relates to an isolated antibody or antibody portion capable  
 CC of specifically binding to or elicited by at least one epitope of a  
 CC heparanase protein, where the heparanase protein is at least 60%  
 CC homologous to any of the 6 sequences given as SEQ ID NOS: 1-5 or 11, and  
 CC where at least one epitope comprises a sequence at least 70% homologous  
 CC to any of the sequences given as SEQ ID NOS: 6-10. Also disclosed are (a)  
 CC a hybridoma cell line comprising a cell line for producing the monoclonal  
 CC antibody, (b) a method for detecting, treating or preventing a  
 CC pathological condition or a heparanase-related disorder or condition in a  
 CC subject, (c) a method for monitoring the state of a heparanase-related  
 CC disorder or condition in a subject, and (d) a pharmaceutical composition  
 CC comprising the isolated anti-heparanase antibody or antibody portion and  
 CC a pharmaceutical carrier. The antibody, methods, and composition are  
 CC useful for detecting, treating, preventing or monitoring a pathological  
 CC condition, e.g. angiogenesis, cell proliferation, a cancerous condition  
 CC (blood, breast, bladder, rectum, stomach, cervix, ovarian, colon, renal,  
 CC or prostate cancer), minor cell proliferation, invasion of circulating

CC tumour cells, or a metastatic disease, or a heparanase-related disorder  
 CC or condition, e.g. an inflammatory disorder, wound, scar, vasculopathy  
 CC (atherosclerosis, restenosis, or aneurysm), autoimmune condition, or  
 CC renal disease or disorder (diabetic nephropathy, glomerulosclerosis,  
 CC nephrotic syndrome, minimal change nephrotic syndrome, or a renal cell  
 CC carcinoma) in a mammal. This sequence represents human heparanase.  
 XX  
 SQ Sequence 543 AA;  
 Query Match 100.0%; Score 2841; DB 8; Length 543;  
 Best Local Similarity 100.0%; Pred. No. 3e-275;  
 Matches 543; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MLLRSKPALPPPLMLLLGLPLSPGALPPPAQAQVVDLDFDFTQEPHLHVSFSLV 60  
 DB 1 MLLRSKPALPPPLMLLLGLPLSPGALPPPAQAQVVDLDFDFTQEPHLHVSFSLV 60  
 QY 61 IDANLATDPRFLIILGSPKRLTARGLSPAYLRFGGTKTDFLIIDPKKESTFEERSY 120  
 DB 61 IDANLATDPRFLIILGSPKRLTARGLSPAYLRFGGTKTDFLIIDPKKESTFEERSY 120  
 QY 121 QVNODICKYGSIPPDVEKLEWYQEOILLREHYQKKFNSTYSRSSVDVLYTFANCS 180  
 DB 121 QVNODICKYGSIPPDVEKLEWYQEOILLREHYQKKFNSTYSRSSVDVLYTFANCS 180  
 QY 181 GLDLIFGLNALLRTADLQWSSNAQLLDYCSSKGYNISWELGNEPNSFLKADIFINGS 240  
 DB 181 GLDLIFGLNALLRTADLQWSSNAQLLDYCSSKGYNISWELGNEPNSFLKADIFINGS 240  
 QY 241 QLGEDFTQLHKLKSTFKNAKLYGPDVGQPRRTAKMLKSFLLKAGGEVIDSVTWHHYL 300  
 DB 241 QLGEDFTQLHKLKSTFKNAKLYGPDVGQPRRTAKMLKSFLLKAGGEVIDSVTWHHYL 300  
 QY 301 NGRTATREDFLNPDVLDIFISSVQKVFQVVESTPGKKVWLGETSSAYGGGAPLLSDTFA 360  
 DB 301 NGRTATREDFLNPDVLDIFISSVQKVFQVVESTPGKKVWLGETSSAYGGGAPLLSDTFA 360  
 QY 361 AGFMWLDKLGLSARMGIEVVMRQVFFGAGNHLVDENFDPLDPYWLSSLFKLVGTVKVL 420  
 DB 361 AGFMWLDKLGLSARMGIEVVMRQVFFGAGNHLVDENFDPLDPYWLSSLFKLVGTVKVL 420  
 QY 421 ASVQGSKRRLRVYVYLHCTNTDNPRYKEDLTLYAINLHNVTYLRLLPYFPFNKQVDKYL 480  
 DB 421 ASVQGSKRRLRVYVYLHCTNTDNPRYKEDLTLYAINLHNVTYLRLLPYFPFNKQVDKYL 480  
 QY 481 RPLGPHGLSKSVQLNGLTWKWDDQTLPLMEKPLRPGSSGLGPAFSYSPFVIRNAKVA 540  
 DB 481 RPLGPHGLSKSVQLNGLTWKWDDQTLPLMEKPLRPGSSGLGPAFSYSPFVIRNAKVA 540  
 QY 541 ACI 543  
 DB 541 ACI 543  
 RESULT 12  
 ADY27036  
 ID ADY27036 standard; protein; 543 AA.  
 XX  
 AC ADY27036;  
 XX  
 DT 05-MAY-2005 (first entry)  
 XX  
 DE Human heparanase protein.  
 XX  
 KW Heparanase; cancer; neoplasm; inflammation; cardiovascular disease;  
 KW neurological disease; viral infection; infection; cytostatic;  
 KW antiinflammatory; cardiovascular-gen.; neuroprotective; virucide;  
 KW protease; enzyme; enzyme purification.  
 XX  
 OS Homo sapiens.  
 XX  
 FN WO2005016227-A2.  
 XX

PD 24-FEB-2005.  
XX 12-AUG-2004; 2004WO-IL000744.  
PF 14-AUG-2003; 2003US-0494800P.  
PR 12-JAN-2004; 2004US-0535492P.  
XX (INSI-) INSIGHT BIOPHARMACEUTICALS LTD.  
XX Van-Gelder JM, Miron D;  
XX WPI; 2005-182203/19.  
DR  
XX  
XX Regulating heparanase activity, useful for treating heparanase-associated  
XX diseases (e.g. cancer, inflammation, cardiovascular diseases,  
PT neurological diseases or viral diseases) comprises modulating heparanase  
PT activation.  
XX  
XX Disclosure; SEQ ID NO 8; 211pp; English.  
XX  
XX The invention relates to a method of regulating heparanase activity in a  
XX tissue or regulating a biological process depending at least in part on  
CC heparanase activity comprising modulating heparanase activation. The  
CC invention also relates to methods of treating a heparanase- or heparin  
CC binding protein-associated disease or disorder in a subject, a  
CC pharmaceutical composition for use in the treatment of a heparanase-  
CC associated disease or disorder comprising a therapeutic amount of an  
CC agent capable of modulating heparanase activation and a pharmaceutical  
CC carrier or diluent, a method of identifying a protease activator of  
CC heparanase, a protease substrate mimetic comprising a peptide  
CC representing a subset or all substrate residues or cleavage sites of  
CC human heparanase or an equivalent non-human heparanase, a method of  
CC producing active heparanase and a method of modulating an adhesion  
CC activity of heparanase. The composition and methods are useful for  
CC modulating heparanase activation and for treating heparanase-associated  
CC diseases or disorders such as cancer, inflammation, cardiovascular  
CC diseases, neurological diseases or viral infections. This sequence  
CC represents a human heparanase protein used in the scope of the invention.  
XX  
XX Sequence 543 AA;  
XX  
XX Query Match 100.0%; Score 2841; DB 9; Length 543;  
XX Best Local Similarity 100.0%; Pred. No. 3e-275;  
XX Matches 543; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MLRSKPALPPMLMLLLGLPLSPGALPRPAQAQDVVDLDFFTQEPHLVSPFLSVT 60  
DB 1 MLRSKPALPPMLMLLLGLPLSPGALPRPAQAQDVVDLDFFTQEPHLVSPFLSVT 60  
QY 61 IDANLATDPRFLILGSPKLRTLARGSPAYLRFSGTKTDFLIDPKKESTFEERSYQWS 120  
DB 61 IDANLATDPRFLILGSPKLRTLARGSPAYLRFSGTKTDFLIDPKKESTFEERSYQWS 120  
QY 121 QVNQDICKYGSIPDPVEEKRLLEWYQEOQLLREHYQKFKNSTYRSRSDVLYTFPANC 180  
DB 121 QVNQDICKYGSIPDPVEEKRLLEWYQEOQLLREHYQKFKNSTYRSRSDVLYTFPANC 180  
QY 181 GLDLIFGLNALLRTADLQWSSNAQLLDYCSKSGYNISWELGNEPNSFLKKADIFPINGS 240  
DB 181 GLDLIFGLNALLRTADLQWSSNAQLLDYCSKSGYNISWELGNEPNSFLKKADIFPINGS 240  
QY 241 QLGEDFIQLHKLKRSKTFKNAKLYGPDVGQPRKRTAKMLKSFLLKAGEVIDSVTHHYHL 300  
DB 241 QLGEDFIQLHKLKRSKTFKNAKLYGPDVGQPRKRTAKMLKSFLLKAGEVIDSVTHHYHL 300  
QY 301 NGRTATREDPLNDVLDIFISSVQKVPQVVESTRPGKKVWLGETSSAYCGGAPLLSDTFA 360  
DB 301 NGRTATREDPLNDVLDIFISSVQKVPQVVESTRPGKKVWLGETSSAYCGGAPLLSDTFA 360  
QY 361 AGFMWLDKGLSARMGIEVVMRQVFFGAGNYHLVDENFDPLPDYWLSSLFPKLVGTVKVL 420  
DB 361 AGFMWLDKGLSARMGIEVVMRQVFFGAGNYHLVDENFDPLPDYWLSSLFPKLVGTVKVL 420

QY 421 ASVOGSKRRKLRVYLHCTNTDNPYKGGDLTLVAINLHNVTKYLRLPYPSNKQVDKYLL 480  
DB 421 ASVOGSKRRKLRVYLHCTNTDNPYKGGDLTLVAINLHNVTKYLRLPYPSNKQVDKYLL 480  
QY 481 RPLGPHGLLSKSVQNLGLTLKMWDDQTLPLMEKPLRPGSLGPAFYSFFVIRNAKVA 540  
DB 481 RPLGPHGLLSKSVQNLGLTLKMWDDQTLPLMEKPLRPGSLGPAFYSFFVIRNAKVA 540  
QY 541 ACI 543  
DB 541 ACI 543  
RESULT 13  
ID AEA42426 standard; protein; 543 AA.  
XX AEA42426;  
XX 28-JUL-2005 (first entry)  
XX Human heparanase protein SEQ ID NO:4.  
XX antibody; heparanase; antiinflammatory; vulnerary; immunosuppressive;  
KW antiangiogenic; cytostatic; antiarteriosclerotic; vasotropic;  
KW inflammation; wound healing; scarring; vasculopathy; autoimmune disease;  
KW angiogenesis disorder; cancer; tumor; metastasis.  
XX Homo sapiens.  
XX  
XX Key Location/Qualifiers  
FT Peptide 89..107  
FT Peptide /note= "heparanase epitope SEQ ID NO:7"  
FT Peptide 219..233  
FT Misc-difference 246 /note= "heparanase epitope SEQ ID NO:8"  
FT Peptide /note= "encoded by TAT"  
FT Peptide 294..307 /note= "heparanase epitope SEQ ID NO:10"  
FT Peptide 334..348 /note  
FT Peptide 437..446  
FT Peptide /note= "heparanase epitope SEQ ID NO:6"  
XX AU2004201462-A1.  
XX 06-MAY-2004.  
XX 08-APR-2004; 2004AU-00201462.  
XX 08-APR-2004; 2004AU-00201462.  
XX (INSI-) INSIGHT BIOPHARMACEUTICALS LTD.  
XX (HADA-) HADASIT MEDICAL RES SERVICES & DEV LTD.  
XX Vlodavsky I, Pecker I, Miron M, Gilboa A, Miron D, Moskowitz H;  
XX Shlomi Y, Peleg Y, Yacoby-Zeevi O, Ayal-Hershkovitz M, Ben-Artzi H;  
XX Feinstein E;  
XX WPI; 2005-173343/19.  
XX N-PSDB; AEA42434, AEA42435, AEA42460.  
XX Novel isolated antibody capable of specifically binding to epitope of  
XX heparanase protein, useful for preventing and treating heparanase-related  
PT disorder such as inflammatory disorder, scars, autoimmune conditions or  
PT angiogenesis.  
XX Claim 2; SEQ ID NO 4; 260pp; English.  
XX The invention relates to an isolated antibody or its portion (I) capable  
CC of specifically binding to an epitope of a heparanase protein. Also  
CC described: (1) a cell line (II) for producing a monoclonal antibody or  
CC its portion, comprising a cell line for producing (I); (2) a

CC pharmaceutical composition comprising (I) and a carrier; and (3) an  
CC affinity medium (III) for binding human heparanase polypeptides,  
CC comprising (I) immobilized to a chemically inert, insoluble carrier. (I)  
CC useful for treating a subject suffering from a pathological condition,  
CC which involves administering (I) to the subject. (I) is useful for  
CC preventing and treating heparanase-related disorder or condition chosen  
CC from inflammatory disorder, wound, scar, vasculopathy, autoimmune  
CC condition, angiogenesis, cell proliferation, cancerous condition, tumor  
CC cell proliferation, invasion of circulating tumor cells and metastatic  
CC disease. (I) is useful for detecting the presence of heparanase  
CC polypeptide in a sample. (I) is useful for detecting heparanase-related  
CC disease or condition in a subject such as vertebrate, preferably mammal  
CC e.g., human. The heparanase-related disorder or condition further  
CC includes renal disease or disorder chosen from diabetic nephropathy,  
CC glomerulosclerosis, nephrotic syndrome, minimal change nephrotic syndrome  
CC and renal cell carcinoma. The present sequence represents human  
CC heparanase, which is used in the exemplification of the present  
CC invention.

XX SQ Sequence 543 AA;

Query Match 100.0%; Score 2841; DB 9; Length 543;  
Best Local Similarity 100.0%; Pred. No. 3e-275;  
Matches 543; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLRSKPALPPPLMLLLGLPLSPGALPPRAQAQDVVDLDFFTQEPHLVSPSFLSVT 60  
DB 1 MLLRSKPALPPPLMLLLGLPLSPGALPPRAQAQDVVDLDFFTQEPHLVSPSFLSVT 60  
QY 61 IDANLATDPRFLILGLSPKLTARGLSPAYLRPGTKTDFLI FDPKKESTFEERSYQWS 120  
DB 61 IDANLATDPRFLILGLSPKLTARGLSPAYLRPGTKTDFLI FDPKKESTFEERSYQWS 120  
QY 121 QVNQDICKYGSIPPDVEEKLRLWPYQOELLRLREHYQKFKNSTYSRSSVDVLYTFANCS 180  
DB 121 QVNQDICKYGSIPPDVEEKLRLWPYQOELLRLREHYQKFKNSTYSRSSVDVLYTFANCS 180  
QY 181 GLDLIFGLNALRLTADLQWNSNAQLLDYCSKGYNISWELGNEPNSFLKKADIFINGS 240  
DB 181 GLDLIFGLNALRLTADLQWNSNAQLLDYCSKGYNISWELGNEPNSFLKKADIFINGS 240  
QY 241 QLGEDFIQLHLLKRLSTFNKALYGPDVQGPQRRTAKMLKSPFKAGGEVIDSVTWHYYL 300  
DB 241 QLGEDFIQLHLLKRLSTFNKALYGPDVQGPQRRTAKMLKSPFKAGGEVIDSVTWHYYL 300  
QY 301 NGRATREDFLNPDLVDFISSVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQV 360  
DB 301 NGRATREDFLNPDLVDFISSVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQV 360  
QY 361 AGFMWLDKGLSARMGIEVWVRQVFFGAGNYHLVDENFDPLDYWLSLLFKLVGTQVLM 420  
DB 361 AGFMWLDKGLSARMGIEVWVRQVFFGAGNYHLVDENFDPLDYWLSLLFKLVGTQVLM 420  
QY 421 ASVQSKRRKRLRVYLHCTNTDNPRYKEGDLTYALNHNVTKYLRPLPYFNSKQVDKYL 480  
DB 421 ASVQSKRRKRLRVYLHCTNTDNPRYKEGDLTYALNHNVTKYLRPLPYFNSKQVDKYL 480  
QY 481 RPLGPHGLLSKVSQVNLGLTKMVDQTLPLMEKPLRPGSSGLGLPAFYSFVIRNAKVA 540  
DB 481 RPLGPHGLLSKVSQVNLGLTKMVDQTLPLMEKPLRPGSSGLGLPAFYSFVIRNAKVA 540  
QY 541 ACI 543  
DB 541 ACI 543  
RESULT 14  
ID AAY30124  
XX AAY30124 standard; protein; 588 AA.  
AC AAY30124;  
XX AAY30124;  
DT 20-MAR-2003 (revised)

DT 14-OCT-1999 (first entry)  
XX A human protein with heparanase activity.  
DE Human; heparanase; heparan sulfate; trauma; autoimmune disease;  
KW skin disease; cardiovascular disease; nervous system disease;  
KW Alzheimer's disease; cancer; cancer metastasis; angiogenesis;  
KW inflammation; arthritis.  
OS Homo sapiens.  
XX WO9940207-A1.  
PN 12-AUG-1999.  
XX 05-FEB-1999; 99WO-EP000777.  
PF 09-FEB-1999; 98GB-00002725.  
PR (NOVS ) NOVARTIS AG.  
PA (NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH.  
XX Nakajima M, Toyoshima M;  
PI WPI; 1999-494300/41.  
DR N-PSDB; AAX86671.  
XX New heparanase polypeptide useful for treating autoimmune diseases, skin  
PT diseases, cardiovascular diseases and nervous system diseases including  
PT Alzheimer's disease.  
PS Claim 3; Page 29-31; 40pp; English.  
XX The present sequence represents a polypeptide with human heparanase  
CC biological activity. Antagonists and inhibitors of the protein prevent it  
CC from degrading the extracellular matrix and releasing heparan sulfate  
CC from the extracellular matrix surface. The heparanase protein or the anti  
CC -heparanase antibody are used in pharmaceutical compositions for treating  
CC warm blooded animals suffering from a disease resulting from shortage or  
CC lack of the heparanase protein, or from excessive activity or over-  
CC expression of the heparanase protein, respectively. The heparanase  
CC protein is used in treating diseases such as trauma, autoimmune disease,  
CC skin diseases, cardiovascular diseases and nervous system diseases  
CC including Alzheimer's disease resulting from shortage or lack of  
CC polypeptide. The anti-heparanase antibody is used in treating the  
CC diseases like cancer, cancer metastasis, angiogenesis and inflammation  
CC including arthritis resulting from excessive activity or over expression  
CC of heparanase protein. The anti-heparanase antibody can be used to detect  
CC the presence or absence of polypeptide and its concentration. (Updated on  
CC 20-MAR-2003 to correct PA field.)  
XX SQ Sequence 588 AA;

Query Match 100.0%; Score 2841; DB 2; Length 588;  
Best Local Similarity 100.0%; Pred. No. 3.5e-275;  
Matches 543; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLRSKPALPPPLMLLLGLPLSPGALPPRAQAQDVVDLDFFTQEPHLVSPSFLSVT 60  
DB 46 MLLRSKPALPPPLMLLLGLPLSPGALPPRAQAQDVVDLDFFTQEPHLVSPSFLSVT 105  
QY 61 IDANLATDPRFLILGLSPKLTARGLSPAYLRPGTKTDFLI FDPKKESTFEERSYQWS 120  
DB 106 IDANLATDPRFLILGLSPKLTARGLSPAYLRPGTKTDFLI FDPKKESTFEERSYQWS 165  
QY 121 QVNQDICKYGSIPPDVEEKLRLWPYQOELLRLREHYQKFKNSTYSRSSVDVLYTFANCS 180  
DB 166 QVNQDICKYGSIPPDVEEKLRLWPYQOELLRLREHYQKFKNSTYSRSSVDVLYTFANCS 225  
QY 181 GLDLIFGLNALRLTADLQWNSNAQLLDYCSKGYNISWELGNEPNSFLKKADIFINGS 240  
DB 226 GLDLIFGLNALRLTADLQWNSNAQLLDYCSKGYNISWELGNEPNSFLKKADIFINGS 285

QY 241 QLGEDFIQLHLKLRKSTFKNAKLYGPDYGVOPRRKTA KMLKSPFKAGGEVIDSVTWHYYL 300  
DB 286 QLGEDFIQLHLKLRKSTFKNAKLYGPDYGVOPRRKTA KMLKSPFKAGGEVIDSVTWHYYL 345  
QY 301 NGRTATREDFLNPDVLDIFISSVQKVFQVVESTRPCKKVLGETSSAYGGAPLLSDTFA 360  
DB 346 NGRTATREDFLNPDVLDIFISSVQKVFQVVESTRPCKKVLGETSSAYGGAPLLSDTFA 405  
QY 361 AGFMWLDKLGLSARMGIEVVMRQVFFGAGNYHLVDENFDPLDPDYWLSLLFKLVGTKVLM 420  
DB 406 AGFMWLDKLGLSARMGIEVVMRQVFFGAGNYHLVDENFDPLDPDYWLSLLFKLVGTKVLM 465  
QY 421 ASVOGSKRRKRLVYLHCTNTDNPRYKEGDLTIYALNHNVTYLRPLVPFSNKQVDKYL 480  
DB 466 ASVOGSKRRKRLVYLHCTNTDNPRYKEGDLTIYALNHNVTYLRPLVPFSNKQVDKYL 525  
QY 481 RPLGPHGLLSKSVQLNGLTLKMWDDQTLPLPMEKPLRPGSSILGLPAFSYFFVIRNAKVA 540  
DB 526 RPLGPHGLLSKSVQLNGLTLKMWDDQTLPLPMEKPLRPGSSILGLPAFSYFFVIRNAKVA 585  
QY 541 ACI 543  
DB 586 ACI 588  
RESULT 15  
AA02345  
ID AA02345 standard; protein; 543 AA.  
AC AA02345;  
XX  
DT 09-JUL-1999 (first entry)  
XX  
DE A human heparanase protein.  
XX  
KW Heparanase; hp; modulator; heparin-binding growth factor;  
KW cellular response; cytokine; cell interaction; plasma lipoprotein;  
KW cellular susceptibility; infection; disintegration;  
KW neurodegenerative plaque; wound healing; angiogenesis; restenosis;  
KW atherosclerosis; inflammation; neurodegenerative disease; neutralise;  
KW plasma heparin; micrometastasis; autoimmune lesion; renal failure.  
XX  
OS Homo sapiens.  
XX  
PN WO9911798-A1.  
XX  
PD 11-MAR-1999.  
XX  
PF 31-AUG-1998; 98WO-US017954.  
XX  
XX 02-SEP-1997; 97US-00922170.  
PR 02-JUL-1998; 98US-00109386.  
XX  
PA (INSI-) INSTIGHT STRATEGY & MARKETING LTD.  
PA (HADA-) HADASIT MEDICAL RES SERVICES & DEV.  
PA (FRIE/) FRIEDMAN M M.  
XX  
PI Pecker I, Vlodavsky I, Feinstein E;  
XX  
XX WPI; 1999-302255/25.  
DR N-PSDB; AAX35648.  
XX  
XX New human polynucleotide useful for treating angiogenesis, restenosis,  
PT and inflammation.  
XX  
XX Claim 6; Fig 1; 63pp; English.  
XX

CC conditions such as wound healing, angiogenesis, restenosis,  
CC atherosclerosis, inflammation, neurodegenerative diseases, and viral  
CC infections. Mammalian heparanase can be used to neutralize plasma  
CC heparin, and anti-heparanase antibodies may be applied for  
CC immunodetection and diagnosis of micrometastases, autoimmune lesions, and  
CC renal failure in biopsy specimens, plasma samples, and body fluids. The  
CC present sequence represents human heparanase  
XX  
SQ Sequence 543 AA;  
Query Match 99.9%; Score 2838; DB 2; Length 543;  
Best Local Similarity 99.8%; Pred. No. 6.1e-275;  
Matches 542; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MLLRSKPALPPLMLLLGPIGPIGSPGALPRPAQADVDLDDFFTQEPHLHLVSPFLSVT 60  
DB 1 MLLRSKPALPPLMLLLGPIGPIGSPGALPRPAQADVDLDDFFTQEPHLHLVSPFLSVT 60  
QY 61 IDANLATDPRFLILLLGSPKRLTLARGLSPAYLRFGGTKTDFLI FDPKKESTFEERSYMQS 120  
DB 61 IDANLATDPRFLILLLGSPKRLTLARGLSPAYLRFGGTKTDFLI FDPKKESTFEERSYMQS 120  
QY 121 QVNQDICKYGSIPDPVEEKRLWPYQBLRLREHYQKKFNKSTYSRSVDVLYTFANC 180  
DB 121 QVNQDICKYGSIPDPVEEKRLWPYQBLRLREHYQKKFNKSTYSRSVDVLYTFANC 180  
QY 181 GLDLIFGLNALLRTADLQWSSNAQLLLDYCSSKGYNISWELGNEPNSFLKKADIFINGS 240  
DB 181 GLDLIFGLNALLRTADLQWSSNAQLLLDYCSSKGYNISWELGNEPNSFLKKADIFINGS 240  
QY 241 QLGEDFIQLHLKLRKSTFKNAKLYGPDYGVOPRRKTA KMLKSPFKAGGEVIDSVTWHYYL 300  
DB 241 QLGEDFIQLHLKLRKSTFKNAKLYGPDYGVOPRRKTA KMLKSPFKAGGEVIDSVTWHYYL 300  
QY 301 NGRTATREDFLNPDVLDIFISSVQKVFQVVESTRPCKKVLGETSSAYGGAPLLSDTFA 360  
DB 301 NGRTATREDFLNPDVLDIFISSVQKVFQVVESTRPCKKVLGETSSAYGGAPLLSDTFA 360  
QY 361 AGFMWLDKLGLSARMGIEVVMRQVFFGAGNYHLVDENFDPLDPDYWLSLLFKLVGTKVLM 420  
DB 361 AGFMWLDKLGLSARMGIEVVMRQVFFGAGNYHLVDENFDPLDPDYWLSLLFKLVGTKVLM 420  
QY 421 ASVOGSKRRKRLVYLHCTNTDNPRYKEGDLTIYALNHNVTYLRPLVPFSNKQVDKYL 480  
DB 421 ASVOGSKRRKRLVYLHCTNTDNPRYKEGDLTIYALNHNVTYLRPLVPFSNKQVDKYL 480  
QY 481 RPLGPHGLLSKSVQLNGLTLKMWDDQTLPLPMEKPLRPGSSILGLPAFSYFFVIRNAKVA 540  
DB 481 RPLGPHGLLSKSVQLNGLTLKMWDDQTLPLPMEKPLRPGSSILGLPAFSYFFVIRNAKVA 540  
QY 541 ACI 543  
DB 541 ACI 543  
Search completed: February 27, 2006, 17:46:54  
Job time : 190 secs



GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioacceleration Ltd.  
OM nucleic - nucleic search, using sw model  
Run on: February 28, 2006, 04:40:00 ; Search time 1068 Seconds  
(without alignments)  
10739.640 Million cell updates/sec  
Title: SEQ1-799T  
Perfect score: 1721  
Sequence: 1 ctgaggtttctgactctcg.....atatactagtcctgacactg 1721  
Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0  
Searched: 4996997 seqs, 332346308 residues  
Total number of hits satisfying chosen parameters: 9993994  
Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_21.\*  
1: Geneseqn1980s.\*  
2: Geneseqn1990s.\*  
3: Geneseqn2000s.\*  
4: Geneseqn2001as.\*  
5: Geneseqn2001bs.\*  
6: Geneseqn2002as.\*  
7: Geneseqn2002bs.\*  
8: Geneseqn2003as.\*  
9: Geneseqn2003bs.\*  
10: Geneseqn2003cs.\*  
11: Geneseqn2003ds.\*  
12: Geneseqn2004as.\*  
13: Geneseqn2004bs.\*  
14: Geneseqn2005s.\*  
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES						
Result No.	Score	Query Match	Length	DB	ID	Description
1	1719.4	99.9	1721	2	AAX35648	Human enco
2	1719.4	99.9	1721	3	AAZ39195	Human hep
3	1719.4	98.9	1721	3	AAZ75051	cDNA enco
4	1719.4	99.9	1721	3	AAX33290	Human hep
5	1719.4	99.9	1721	4	AAZ91112	Human hep
6	1719.4	99.9	1721	10	ADG88801	Human tpa
7	1719.4	99.9	1721	10	ADG88799	Human tpa
8	1719.4	99.9	1721	12	ADL16380	Human hep
9	1719.4	99.9	1721	12	ADL16378	Human hep
10	1719.4	98.9	1721	12	ADM48717	Human tpa
11	1719.4	99.9	1721	12	ADM48715	Human tpa
12	1719.4	99.9	1721	14	AEA42434	Human hep
13	1719.4	99.9	1721	14	AEA42435	Human hep
14	1717.8	99.8	1899	2	AAX35650	cDNA enco
15	1717.8	99.8	1899	3	AAZ75053	cDNA enco
16	1717.8	99.8	1899	10	ADG88803	Human SK-
17	1717.8	99.8	1899	10	ADG88805	Human SK-
18	1717.8	99.8	1899	12	ADL16384	Human hep
19	1717.8	99.8	1899	12	ADL16382	Human hep

20	1717.8	99.8	1899	12	ADM48719						
21	1717.8	99.8	1899	12	ADM48721						
22	1717.8	99.8	1899	14	AEA42460						
23	1714.6	99.6	1722	5	AAF93788						
24	1714.6	99.6	1722	14	ADY63086						
25	1699.4	98.7	1701	14	AEA42485						
26	1696.2	98.6	1713	2	AAX37259						
27	1690.4	98.2	1723	2	AAX37260						
28	1688.4	98.1	3726	2	AAX86671						
29	1688.4	98.1	3726	10	ADL18951						
30	1688.4	98.1	3726	12	ADK51968						
31	1688.4	98.1	3726	12	ADN04901						
32	1688.4	98.1	3726	12	ADN05073						
33	1688.4	98.1	3726	13	ADQ80253						
34	1688.4	98.1	3726	13	ADP25078						
35	1684.2	97.9	1724	4	AAH20940						
36	1649.6	95.9	1673	12	ADO63816						
37	1649.6	95.9	1673	12	ADO63817						
38	1648	95.8	1673	12	ADO63818						
39	1633	94.9	1669	8	ABZ22816						
40	1633	94.9	1669	10	ADE16011						
41	1631.4	94.8	1669	12	ADL93950						
42	1586.6	92.2	1593	2	AAZ11236						
43	1578.4	91.7	1668	14	ADZ19009						
44	1555.8	90.4	1625	12	ADO63819						
45	1555.8	90.4	1625	12	ADO63820						

ALIGNMENTS

RESULT 1

AAX35648

ID AAX35648 standard; cDNA; 1721 BP.

AC AAX35648;

XX 09-JUL-1999 (first entry)

XX cDNA encoding a human heparanase protein.

DE Heparanase; hpa; modulator; heparin-binding growth factor;  
KW cellular response; cytokine; cell interaction; plasma lipoprotein;  
KW cellular susceptibility; infection; disintegration;  
KW neurodegenerative plaque; wound healing; angiogenesis; restenosis;  
KW atherosclerosis; inflammation; neurodegenerative disease; neutralise;  
KW plasma heparin; micrometastasis; autoimmune lesion; renal failure; ss.  
XX Homo sapiens.  
OS  
XX WO9911798-A1.  
FN  
XX 11-MAR-1999.  
PD  
XX 31-AUG-1998; 98WO-US017954.  
PF  
XX 02-SEP-1997; 97US-00922170.  
PR  
XX 02-JUL-1998; 98US-00109386.  
PR  
XX (INSI-) INSIGHT STRATEGY & MARKETING LTD.  
PA (HADA-) HADASIT MEDICAL RES SERVICES & DEV.  
PA (FRIE/) FRIEDMAN M M.  
PI Pecker I, Vlodavsky I, Feinstein B;  
XX  
XX WPI; 1999-302255/25.  
DR P-PSDB; AAY02345.  
XX  
XX New human polynucleotide useful for treating angiogenesis, restenosis,  
PT and inflammation.  
XX  
XX Claim 4; Fig 1; 63pp; English.  
PS  
XX

CC The specification describes a polypeptide having heparanase (hpa)  
CC activity. The recombinant protein is used as a modulator of heparin-  
CC binding growth factors, cellular responses to heparin-binding growth  
CC factors and cytokines, cell interaction with plasma lipoproteins,  
CC cellular susceptibility to viral, protozoal and bacterial infections or  
CC disintegration of neurodegenerative plaques. Heparanase may be useful for  
CC conditions such as wound healing, angiogenesis, restenosis,  
CC atherosclerosis, inflammation, neurodegenerative diseases, and viral  
CC infections. Mammalian heparanase can be used to neutralize plasma  
CC heparin, and anti-heparanase antibodies may be applied for  
CC immunodetection and diagnosis of micrometastases, autoimmune lesions, and  
CC renal failure in biopsy specimens, plasma samples, and body fluids. The  
CC present sequence encodes human heparanase  
XX  
SQ

Sequence 1721 BP; 451 A; 413 C; 410 G; 447 T; 0 U; 0 Other;

Query Match 99.9%; Score 1719.4; DB 2; Length 1721;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 1720; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	1	CTAGAGCTTTGCACTCCGCTGCGCGCAGCTGGCGGGGGAGCAGCCAGGTGAGCCCA	60
Db	1	CTAGAGCTTTGCACTCCGCTGCGCGCAGCTGGCGGGGGAGCAGCCAGGTGAGCCCA	60
Qy	61	AGATGCTGCTGCGCTCGAAGCCTGGCTGCGCGCGCGCTGATGCTGCTCTGGGGC	120
Db	61	AGATGCTGCTGCGCTCGAAGCCTGGCTGCGCGCGCGCTGATGCTGCTCTGGGGC	120
Qy	121	CGCTGGGTCCTCTCCCTGGCGCCTGCGCGCGCGCTGATGCTGCTCTGGGGC	180
Db	121	CGCTGGGTCCTCTCCCTGGCGCCTGCGCGCGCGCTGATGCTGCTCTGGGGC	180
Qy	181	ACCTGGAGCTTTTACCCAGAGCGCTGACCTGGTGGGCGCCCTCTCTGTCCTGCA	240
Db	181	ACCTGGAGCTTTTACCCAGAGCGCTGACCTGGTGGGCGCCCTCTCTGTCCTGCA	240
Qy	241	CCATTGACGCAACTGGCCACGACCGCGGTTCTCTATCTCTGGGTTCTCCAAAGC	300
Db	241	CCATTGACGCAACTGGCCACGACCGCGGTTCTCTATCTCTGGGTTCTCCAAAGC	300
Qy	301	TTCTGTAACCTGGCCAGAGGCTTGCTCTCTGGTACCTGAGGTTGGTGCCACCAAGAC	360
Db	301	TTCTGTAACCTGGCCAGAGGCTTGCTCTCTGGTACCTGAGGTTGGTGCCACCAAGAC	360
Qy	361	ACTTCTTAATTTTCGATCCCAAGAGGAATCAACCTTTGAAGAGAGAAATTTACTGGCAAT	420
Db	361	ACTTCTTAATTTTCGATCCCAAGAGGAATCAACCTTTGAAGAGAGAAATTTACTGGCAAT	420
Qy	421	CTCAAGTCAACAGAGATTTTGCAAAATATGATCCATCCCTCTCTGATGTGGAGAGAGT	480
Db	421	CTCAAGTCAACAGAGATTTTGCAAAATATGATCCATCCCTCTCTGATGTGGAGAGAGT	480
Qy	481	TACGGTTGGAAATGGCCCTTACAGGAGCAATTTGCTACTCCGGAACACACTACCCAGAAAAAGT	540
Db	481	TACGGTTGGAAATGGCCCTTACAGGAGCAATTTGCTACTCCGGAACACACTACCCAGAAAAAGT	540
Qy	541	TCAAGACAGACACCTACTCAAGAGCTCTGATGATGCTATACACTTTTGCAACCTGCT	600
Db	541	TCAAGACAGACACCTACTCAAGAGCTCTGATGATGCTATACACTTTTGCAACCTGCT	600
Qy	601	CAGACTGGACTGATCTTTGGCTTAAATGGTTTAAAGAAACAGCAGATTTGCAAGTGA	660
Db	601	CAGACTGGACTGATCTTTGGCTTAAATGGTTTAAAGAAACAGCAGATTTGCAAGTGA	660
Qy	661	ACAGTTCTTAATGCTCAGTTGCTCTGGACTACTGCTCTTCCAGGGGTATAACATTTCTT	720
Db	661	ACAGTTCTTAATGCTCAGTTGCTCTGGACTACTGCTCTTCCAGGGGTATAACATTTCTT	720
Qy	721	GGGAACAGCAATGAACCTAACAGTTTCTTAAGAGGCTGATATTTTCAATCAATGGGT	780
Db	721	GGGAACAGCAATGAACCTAACAGTTTCTTAAAGAGGCTGATATTTTCAATCAATGGGT	780
Qy	781	CGCAGTTAGGAGAGATTTTATTCATTTGCATATAAACTTCTAAGAAAGTCCACCTTCAAAA	840

Db	781	CGCAGTTAGGAGAGATTTATATTAATTCATTAATAAATCTTCTAAGAAAGTCCACCTTCAAAA	840
Qy	841	ATGCAAAACTCTATGTCCTGATGTTGGTTCAGCCTCGAAGAAAGACGGCTAAGATGCTGA	900
Db	841	ATGCAAAACTCTATGTCCTGATGTTGGTTCAGCCTCGAAGAAAGACGGCTAAGATGCTGA	900
Qy	901	AGAGCTTCCTGAAGGCTGGTGGAGAGATGATTCATTCAGTTACATGGCATCACTACTATT	960
Db	901	AGAGCTTCCTGAAGGCTGGTGGAGAGATGATTCATTCAGTTACATGGCATCACTACTATT	960
Qy	961	TGAATGGACGCACTGCTTACCCAGGGAAGATTTTCTTAAACCTCTGATGTTTGAATTTTA	1020
Db	961	TGAATGGACGCACTGCTTACCCAGGGAAGATTTTCTTAAACCTCTGATGTTTGAATTTTA	1020
Qy	1021	TTTCACTGTGCAAAAAGTTTTTCCAGGTGGTGGAGACACAGGCTGGCAAGAGTCT	1080
Db	1021	TTTCACTGTGCAAAAAGTTTTTCCAGGTGGTGGAGACACAGGCTGGCAAGAGTCT	1080
Qy	1081	GGTTAGGAGAAACAAGCTCTGCATATGGAGGCGGAGCGCCCTTGTATCCGACACCTTTG	1140
Db	1081	GGTTAGGAGAAACAAGCTCTGCATATGGAGGCGGAGCGCCCTTGTATCCGACACCTTTG	1140
Qy	1141	CAGCTGGCTTTATGTCGCTGGATAAATTTGGGCTGTGAGCCCGAATGGGAATAGAAGTGG	1200
Db	1141	CAGCTGGCTTTATGTCGCTGGATAAATTTGGGCTGTGAGCCCGAATGGGAATAGAAGTGG	1200
Qy	1201	TGATGAGGCAAGTATCTTTGGAGCGAGAAACTACCACTTTAGTGGATGAAACCTTCGATC	1260
Db	1201	TGATGAGGCAAGTATCTTTGGAGCGAGAAACTACCACTTTAGTGGATGAAACCTTCGATC	1260
Qy	1261	CTTTACCTGATTTTGGCTATCTCTCTGTTCAAGAAATTTGGTGGGCAACCAAGGTGTAA	1320
Db	1261	CTTTACCTGATTTTGGCTATCTCTCTGTTCAAGAAATTTGGTGGGCAACCAAGGTGTAA	1320
Qy	1321	TGGCAAGCGTCAAGGTTCAAAGAGAGGAAGCTTCGAGTATACCTTTCAATTGCACAAACA	1380
Db	1321	TGGCAAGCGTCAAGGTTCAAAGAGAGGAAGCTTCGAGTATACCTTTCAATTGCACAAACA	1380
Qy	1381	CTGACAACTCAAGGTATAAGAGAGGAGATTTAACTCTGATGCAATAAACCTCCATAACG	1440
Db	1381	CTGACAACTCAAGGTATAAGAGAGGAGATTTAACTCTGATGCAATAAACCTCCATAACG	1440
Qy	1441	TCACCAAGTACTTGGGTTACCTCTTCTTCTAACCAAGCAAGTGGATAAATACCTTC	1500
Db	1441	TCACCAAGTACTTGGGTTACCTCTTCTTCTAACCAAGCAAGTGGATAAATACCTTC	1500
Qy	1501	TAAGACCTTTGGGACCTCATGGATTTACTTTCCAAATCTGTCCAACTCAATGGTCTAATC	1560
Db	1501	TAAGACCTTTGGGACCTCATGGATTTACTTTCCAAATCTGTCCAACTCAATGGTCTAATC	1560
Qy	1561	TAAAGATGGTGGATGATCAAACTTGGCACCTTTTAATGGAAAAACCTCTCCGGCAGGAA	1620
Db	1561	TAAAGATGGTGGATGATCAAACTTGGCACCTTTTAATGGAAAAACCTCTCCGGCAGGAA	1620
Qy	1621	GTTCACTGGGCTTGGCAGCTTTCTCATATAGTTTTTTTGTGATAAGAAATGCCAAAGTTG	1680
Db	1621	GTTCACTGGGCTTGGCAGCTTTCTCATATAGTTTTTTTGTGATAAGAAATGCCAAAGTTG	1680
Qy	1681	CTGTTGTCATCTGAAAAATAAATAATATAGTCTCTGACACTG 1721	
Db	1681	CTGTTGTCATCTGAAAAATAAATAATATAGTCTCTGACACTG 1721	

RESULT 2

AAZ39195

ID AAZ39195 standard; cdna; 1721 BP.

XX AAZ39195;

AC AAZ39195;

XX 02-MAR-2000 (first entry)

XX Human heparanase encoding cdna.

DE

XX	Human; heparanase; hpa; genetic modification; expression; anticancer; angiogenesis; anti-angiogenic; antiproliferative; antiviral; antitumour; anti-atherosclerotic; anti-inflammatory; antineurodegeneration;
KW	heparan sulphate; heparin-binding growth factor; tumour angiogenesis;
KW	metastasis; wound healing; restenosis; atherosclerosis; inflammation;
KW	neurodegeneration; viral infection; cystic fibrosis; cancer; diagnosis;
KW	micrometastasis; autoimmune lesion; kidney failure; ss.
XX	Homo sapiens.
OS	
XX	
XX	Key Location/Qualifiers
FF	63..1694
FT	/*tag= a
FT	/product= "heparanase"
FT	
FT	
FT	
FT	
XX	W0957244-Al.
PN	
XX	
XX	11-NOV-1999.
PD	
XX	
XX	29-APR-1999; 99WO-US009256.
FF	
XX	
XX	01-MAY-1998; 98US-00071618.
PR	
PR	02-MAR-1999; 99US-00260038.
XX	
XX	(INSI-) INSIGHT STRATEGY & MARKETING LTD.
PA	(FRIE/) FRIEDMAN M M.
PA	
XX	
PI	Ben-Artzi H, Ayal-HersHKovitz M, Yacoby-Zeevi O, Pecker I;
PI	Peleg Y, Shlomi Y;
PI	
DR	WPI; 2000-062144/05.
DR	P-PSDB; AAY57590.
XX	
XX	Engineered cells that express recombinant heparanase, useful
PT	therapeutically, e.g. for treating angiogenesis and to screen for
PT	specific inhibitors, potential anticancer agents.
XX	
XX	Claim 2; Page 106-107; 118pp; English.
XX	
XX	The present invention describes genetically modified cells (A) containing
CC	a polynucleotide (I) that encodes a polypeptide with heparanase activity,
CC	and express recombinant heparanase (II). Heparanase cleaves heparan
CC	sulphate (HS) at specific intrachain sites, resulting in release of
CC	heparin-binding growth factors, enzymes and proteins that are sequestered
CC	by HS in basement membranes, extracellular matrix or cell surfaces. It
CC	may also be implicated in tumour angiogenesis and metastases. (II) is
CC	potentially useful in wound healing and for treating angiogenesis,
CC	restenosis, atherosclerosis, inflammation, neurodegeneration, viral
CC	infection and cystic fibrosis. It can also be used to neutralise heparin
CC	(an alternative to protamine) and to screen for specific inhibitors
CC	(potentially useful for treating cancer and metastases). Antibodies
CC	raised against (II) are used for immunodetection and diagnosis of
CC	micrometastases, autoimmune lesions and kidney failure. (A) provide (II)
CC	in large quantities, in a form that is homogeneously processed and
CC	activated/neutralised by a dedicated protease. The present sequence
CC	encodes human heparanase
XX	
XX	Sequence 1721 BP; 451 A; 413 C; 410 G; 447 T; 0 U; 0 Other;
SQ	
Query Match	99.9%; Score 1719.4; DB 3; Length 1721;
Best Local Similarity	99.9%; Pred. No. 0;
Matches 1720; Conservative	0; Mismatches 1; Indels 0; Gaps 0;
Oy	1 CTAGAGCTTTGACTCTCGCTGCGCGGACGCTGGCGGGGAGCAGCCAGGTGAGCCCA 60
Db	1 CTAGAGCTTTGACTCTCGCTGCGCGGACGCTGGCGGGGAGCAGCCAGGTGAGCCCA 60
Oy	61 AGATGCTGCTGGCGTCGAAGCGTGGCTGCCCGCGCGCTGATGCTGCTCTCTGGGGC 120
Db	61 AGATGCTGCTGGCGTCGAAGCGTGGCTGCCCGCGCGCTGATGCTGCTCTCTGGGGC 120
Oy	121 CGCTGGGTCCTCTCTCCCTGGCGCCCTGGCGCCGACCTGGCAGCAGCAGCGTGTGG 180



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QY 601 CAGGACTGGACTTCATCTTTGGCCCTAAATGCGTTATTAAGAACAGCAGATTTGCGAGTGA 660
Db 601 CAGGACTGGACTTCATCTTTGGCCCTAAATGCGTTATTAAGAACAGCAGATTTGCGAGTGA 660
QY 661 ACAGTTCTAATGCTCAGTCTGCTGAGTACTGCTCTCCNAGGGGTATAACATTTCTT 720
Db 661 ACAGTTCTAATGCTCAGTCTGCTGAGTACTGCTCTCCNAGGGGTATAACATTTCTT 720
QY 721 GGGAACTAGGCAATGAACCTAAACAGATTTTCTTAAGAAAGGCTGATATTTTTCATCAATGGGT 780
Db 721 GGGAACTAGGCAATGAACCTAAACAGATTTTCTTAAGAAAGGCTGATATTTTTCATCAATGGGT 780
QY 781 CGCAGTTAGGAGAAAGATTTTATCAATGTCANAACTTCTAAGAAAGTCCACCTTCAAAA 840
Db 781 CGCAGTTAGGAGAAAGATTTATTAATCAATGTCANAACTTCTAAGAAAGTCCACCTTCAAAA 840
QY 841 ATGCAGAACTCTATGCTGCTGATCTGCTGAGCTCGAAGAAAGACGGCTAAGATGCTGA 900
Db 841 ATGCAGAACTCTATGCTGCTGATCTGCTGAGCTCGAAGAAAGACGGCTAAGATGCTGA 900
QY 901 AGAGCTTCTGAGGCTGGTGGAGAGTGTATTTAGTTTACATGTCATCACTACTATT 960
Db 901 AGAGCTTCTGAGGCTGGTGGAGAGTGTATTTAGTTTACATGTCATCACTACTATT 960
QY 961 TGAATGACGGACTGCTACACAGGGAAGATTTTCTAAACCTGTATGTAATGGAATTTTGA 1020
Db 961 TGAATGACGGACTGCTACACAGGGAAGATTTTCTAAACCTGTATGTAATGGAATTTTGA 1020
QY 1021 TTTTCATCTGCAAAAAGTTTTCAGGTGTTGAGACACCGCCCTGGCAAGAGTCT 1080
Db 1021 TTTTCATCTGCAAAAAGTTTTCAGGTGTTGAGACACCGCCCTGGCAAGAGTCT 1080
QY 1081 GGTTAGGAGAAACAAAGCTCTGCATATGAGCGCGAGCGCTTCTATCCGACACCTTTG 1140
Db 1081 GGTTAGGAGAAACAAAGCTCTGCATATGAGCGCGAGCGCTTCTATCCGACACCTTTG 1140
QY 1141 CAGCTGCTTTATGCTGCTGATTAATTTGGCCCTGTGTCAGCCGCAAGTGAAGTGG 1200
Db 1141 CAGCTGCTTTATGCTGCTGATTAATTTGGCCCTGTGTCAGCCGCAAGTGAAGTGG 1200
QY 1201 TGATGAGGCAAGTATTTCTTGGAGCAGGAATACCATTTAGTGGATGAACCTTCGATC 1260
Db 1201 TGATGAGGCAAGTATTTCTTGGAGCAGGAATACCATTTAGTGGATGAACCTTCGATC 1260
QY 1261 CTTTACCTGATTTATGCTATCTCTCTGTTCAAGAAATTTGGTGGCACCAGAGTGTAA 1320
Db 1261 CTTTACCTGATTTATGCTATCTCTCTGTTCAAGAAATTTGGTGGCACCAGAGTGTAA 1320
QY 1321 TGGCAAGCGTCAAGGTTCAAGAGAGAGGAGCTTCGAGTATACCTTTTCATTCGACAAACA 1380
Db 1321 TGGCAAGCGTCAAGGTTCAAGAGAGAGGAGCTTCGAGTATACCTTTTCATTCGACAAACA 1380
QY 1381 CTGCAATCCAGGTATAAGAGGAGATTTAATCTGTATGCTATGATTAACCTCCATACG 1440
Db 1381 CTGCAATCCAGGTATAAGAGGAGATTTAATCTGTATGCTATGATTAACCTCCATACG 1440
QY 1441 TCACCAAGTACTTCGCGTTACCTCTATCTTTTCAACAGCAAGTGGATAATACCTTC 1500
Db 1441 TCACCAAGTACTTCGCGTTACCTCTATCTTTTCAACAGCAAGTGGATAATACCTTC 1500
QY 1501 TAAGACCTTTGGGACCTCATGGATTTCTTCCAAATCTGTCCTCAATGGTCTAACTC 1560
Db 1501 TAAGACCTTTGGGACCTCATGGATTTCTTCCAAATCTGTCCTCAATGGTCTAACTC 1560
QY 1561 TAAAGATGGTGGATGATCAACCTTGCACCTTTAATGGAAAAACCTCTCCGGCCAGGAA 1620
Db 1561 TAAAGATGGTGGATGATCAACCTTGCACCTTTAATGGAAAAACCTCTCCGGCCAGGAA 1620
QY 1621 GTTCACCTGGGCTGCCAGCTTCTCATATAGTTTTTTTGTATGAAGAAATGCCAAGTTG 1680
Db 1621 GTTCACCTGGGCTGCCAGCTTCTCATATAGTTTTTTTGTATGAAGAAATGCCAAGTTG 1680
QY 1681 CTGCTTGCATCTGAAAAATAAATAATAGTCTGACACTG 1721
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Db 1681 CTGCTTGCATCTGAAAAATAAATAATAGTCTGACACTG 1721
RESULT 4
ID AAZ33290 standard; cDNA; 1721 BP.
XX AAZ33290;
XX 21-FEB-2000 (first entry)
XX Human heparanase nucleotide sequence.
XX Human; heparanase; hpa; diagnosis; therapy; tumour; cytostatic;
XX antidiabetic; immunomodulatory; anti-inflammatory; nephrotropic;
XX metastasis; adenocarcinoma; squamous cell carcinoma; teratocarcinoma;
XX mesothelioma; melanoma; lymphoma; leukemia; cancer; sepsis; diabetes;
XX inflammation; haemorrhagic nephritis; nephrotic syndrome;
XX autoimmune disease; anticancer; kidney disease; ds.
XX Homo sapiens.
XX Key Location/Qualifiers
XX CDS 63..1694
XX FT /*tag= a
XX FT /product= "heparanase"
XX WO9957153-A1.
XX 11-NOV-1999.
XX 29-APR-1999; 99WO-US009255.
XX 01-MAY-1998; 98US-00071739.
XX (INSI-) INSIGHT STRATEGY & MARKETING LTD.
XX (HADA-) HADASIT MEDICAL RES SERVICES & DEV.
XX (FRIE/) FRIEDMAN M M.
XX Pecker I, Vlodavsky I, Friedman Y, Perets T;
XX WPI; 2000-052944/04.
XX P-PSDB; AAY52990.
XX Heparanase-specific molecular probes useful for diagnosis and treatment,
XX e.g. of tumors, and for targeted drug delivery.
XX Example; Page 82-84; 90pp; English.
XX The present invention describes heparanase-specific molecular probes,
XX useful for methods of detecting heparanase in situ. The probes and anti-
XX heparanase antibodies are used to detect or quantify the expression of
XX heparanase, for diagnosis and monitoring of diseases (especially
XX metastasis), for treatment of heparanase-associated diseases (e.g.
XX tumors, (adeno)carcinoma, squamous cell carcinoma, teratocarcinoma,
XX mesothelioma, melanoma, lymphoma or leukemia, a solid cancer for its
XX metastases) derived from liver, prostate, bladder, breast, ovary, cervix,
XX colon, skin, intestine, stomach, uterus and pancreas, kidney disease,
XX diabetes and inflammation, haemorrhagic nephritis, nephrotic syndrome,
XX sepsis and inflammatory or autoimmune disease), for targeted drug
XX delivery (e.g. of anticancer agents) and as research reagents. The
XX present sequence encodes human heparanase, which is used in the
XX exemplification of the present invention
XX SQ Sequence 1721 BP; 451 A; 413 C; 410 G; 447 T; 0 U; 0 Other;
Query Match 99.9%; Score 1719.4; DB 3; Length 1721;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1720; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CTAGAGCTTTGCACTTCGCTCGCGGACGCTGGCGGGGAGCAGCCAGGTGAGCCCA 60
|||||
```

Db 1 CTAGAGCTTTCGACTCTCCGTCGCGCGCAGCTGCGGGGGAGCAGCCAGGTGAGCCCA 60  
Qy  
Db 61 AGATGCTGCTCGCTCGAAGCTCGCTGCGCGCGCGCTGATGCTGCTGCTCGGGGC 120  
Db 61 AGATGCTGCTCGCTCGAAGCTCGCTGCGCGCGCGCTGATGCTGCTGCTCGGGGC 120  
Qy 121 CGCTGGGTCCCTCTCCCTCGCGCCCTGCGCCCGACCTCGCAAGACAGACAGCTCGTGG 180  
Db 121 CGCTGGGTCCCTCTCCCTCGCGCCCTGCGCCCGACCTCGCAAGACAGACAGCTCGTGG 180  
Qy 181 ACCTGGACTTCTTCAACAGAGCGCTGCACTCTGGTGAGCCCTCGTCTGCTGCTGCA 240  
Db 181 ACCTGGACTTCTTCAACAGAGCGCTGCACTCTGGTGAGCCCTCGTCTGCTGCTGCA 240  
Qy 241 CCATGTAGGCCAACTGGCCACGACCGCGGGTTCCTCATCTCTCGGTTCCTCAAGC 300  
Db 241 CCATGTAGCGCAACCTGGCCACGACCGCGGGTTCCTCATCTCTCGGTTCCTCAAGC 300  
Qy 301 TTCTGTACTTGGCCAGAGGCTTGTCTCTCGGTGACCTGAGGTTTGGTGCAACCAAGACAG 360  
Db 301 TTCTGTACTTGGCCAGAGGCTTGTCTCTCGGTGACCTGAGGTTTGGTGCAACCAAGACAG 360  
Qy 361 ACTTCCTAAATTTCCGATCCCAAGAGGAATCAACCTTTGAGAGAGAACTTACTGGCAAT 420  
Db 361 ACTTCCTAAATTTCCGATCCCAAGAGGAATCAACCTTTGAGAGAGAACTTACTGGCAAT 420  
Qy 421 CTCAGTCAACCAAGATATTGGCAATATGATGATCCATCCCTCTGATGTGGAGAGAGT 480  
Db 421 CTCAGTCAACCAAGATATTGGCAATATGATGATCCATCCCTCTGATGTGGAGAGAGT 480  
Qy 481 TACGGTTGGAATGGCCCTACCAAGAGCAATTTGCTACTCCGAGAACACTTACCAGAAAAAGT 540  
Db 481 TACGGTTGGAATGGCCCTACCAAGAGCAATTTGCTACTCCGAGAACACTTACCAGAAAAAGT 540  
Qy 541 TCAAGAACAGCACCTACTCAAGAGCTCTGTAGATGTCTATACACTTTTGCAAACTGCT 600  
Db 541 TCAAGAACAGCACCTACTCAAGAGCTCTGTAGATGTCTATACACTTTTGCAAACTGCT 600  
Qy 601 CAGGACTGGACTTGTATCTTGGCCCTAAATGGCTTTAAGAACAGCAGATTGCGAGTGA 660  
Db 601 CAGGACTGGACTTGTATCTTGGCCCTAAATGGCTTTAAGAACAGCAGATTGCGAGTGA 660  
Qy 661 ACAGTTCTAATGCTCAGTTGCTCTGGACTACTGCTCTTCCAAGGGGTATAAATTTCTT 720  
Db 661 ACAGTTCTAATGCTCAGTTGCTCTGGACTACTGCTCTTCCAAGGGGTATAAATTTCTT 720  
Qy 721 GGGAACTAGGCAATGAACCTAACAGTTTCTTAAAGAGGCTGATATTTCATCAATGGGT 780  
Db 721 GGGAACTAGGCAATGAACCTAACAGTTTCTTAAAGAGGCTGATATTTCATCAATGGGT 780  
Qy 781 CGCAGTTAGGAGAAGATTTTATCAATTGCATATAAATCTTAAGAAAGTCCACCTTCAAAA 840  
Db 781 CGCAGTTAGGAGAAGATTTATCAATTGCATATAAATCTTAAAGAAAGTCCACCTTCAAAA 840  
Qy 841 ATGCAAAACTCTATGGTCTCATGTGTGTGCTGAGCTCGAAGAAAGACGCTAAGATGCTGA 900  
Db 841 ATGCAAAACTCTATGGTCTCATGTGTGTGCTGAGCTCGAAGAAAGACGCTAAGATGCTGA 900  
Qy 901 AGAGCTTCTGAAGGCTGGTGGAGAAGTGTATTGATTACAGTTACATGGCATCACTACTATT 960  
Db 901 AGAGCTTCTGAAGGCTGGTGGAGAAGTGTATTGATTACAGTTACATGGCATCACTACTATT 960  
Qy 961 TGAATGGACGCACTGCTACAGGGAAGATTTTCTAAACCTGTGATTGGACATTTTTTA 1020  
Db 961 TGAATGGACGCACTGCTACAGGGAAGATTTTCTAAACCTGTGATTGGACATTTTTTA 1020  
Qy 1021 TTTTCATCTGTGCAAAAAGTTTTTCCAGGTGGTTGAGACCAAGCTGCGCAAGAGGTCT 1080  
Db 1021 TTTTCATCTGTGCAAAAAGTTTTTCCAGGTGGTTGAGACCAAGCTGCGCAAGAGGTCT 1080  
Qy 1081 GGTTAGGAGAAACAGCTCTGCATATGGAGCGGAGCGCCCTTGTATCCGACACCTTTG 1140  
Db 1081 GGTTAGGAGAAACAGCTCTGCATATGGAGCGGAGCGCCCTTGTATCCGACACCTTTG 1140

Qy 1141 CAGTGGCTTTATGTGGCTGATAAATTTGGCCCTGTGAGCCCGAATGGGAATAGAAAGTGG 1200  
Db 1141 CAGTGGCTTTATGTGGCTGATAAATTTGGCCCTGTGAGCCCGAATGGGAATAGAAAGTGG 1200  
Qy 1201 TGATAGGCAAGTATTCTTTTGGAGCAGGAAACTACATTTAGTGGATGAAAACTTCGATC 1260  
Db 1201 TGATAGGCAAGTATTCTTTTGGAGCAGGAAACTACATTTAGTGGATGAAAACTTCGATC 1260  
Qy 1261 CTTTACCTGATTATTGGCTATCTCTTCTGTTCAAGAAATTTGGTGGGACCAAGGTGTAA 1320  
Db 1261 CTTTACCTGATTATTGGCTATCTCTTCTGTTCAAGAAATTTGGTGGGACCAAGGTGTAA 1320  
Qy 1321 TGCACAGCTGCAAGGTTCAAAGAGAGGAAGCTTCGAGTATACCTTTCATTTGCACAAACA 1380  
Db 1321 TGCACAGCTGCAAGGTTCAAAGAGAGGAAGCTTCGAGTATACCTTTCATTTGCACAAACA 1380  
Qy 1381 CTGACAACTCAAGGTATAAAGAGAGATTTAACTCTGTATGCCATAAACTCCATACG 1440  
Db 1381 CTGACAACTCAAGGTATAAAGAGAGATTTAACTCTGTATGCCATAAACTCCATACG 1440  
Qy 1441 TCACCAAGTACTTGGGTTACCTATCCTTTTCTTCAACAGCAAGTGGATAAATACCTTC 1500  
Db 1441 TCACCAAGTACTTGGGTTACCTATCCTTTTCTTCAACAGCAAGTGGATAAATACCTTC 1500  
Qy 1501 TAAGACCTTTGGACCTCATGGATTACTTTCCAAATCTGTCCAACTCAATGGTCTAACTC 1560  
Db 1501 TAAGACCTTTGGACCTCATGGATTACTTTCCAAATCTGTCCAACTCAATGGTCTAACTC 1560  
Qy 1561 TAAAGATGGTGGATGATCAAACTTGCACCTTTTAATGGAAAACTCTCCGGCCAGGAA 1620  
Db 1561 TAAAGATGGTGGATGATCAAACTTGCACCTTTTAATGGAAAACTCTCCGGCCAGGAA 1620  
Qy 1621 GTTACCTGGGCTTGCAGCTTTCTCATATAGTTTTTTTGTGATAAGAAATGCCAAAGTTG 1680  
Db 1621 GTTACCTGGGCTTGCAGCTTTCTCATATAGTTTTTTTGTGATAAGAAATGCCAAAGTTG 1680  
Qy 1681 CTGCTTGCATCTGAAAATAAATAATATACTAGTCTGCACACTG 1721  
Db 1681 CTGCTTGCATCTGAAAATAAATAATATACTAGTCTGCACACTG 1721

RESULT 5

AAA91112  
ID AAA91112 standard; DNA; 1721 BP.

XX AAA91112;

XX 20-APR-2001 (first entry)

XX Human heparanase, coding sequence fragment isolated from EST clone.

XX Heparanase; hnhp1; wound healing; angiogenesis; restenosis; Scrape;  
XX atherosclerosis; inflammation; pulmonary disease; Alzheimer's disease;  
XX neurodegenerative disease; Creutzfeldt-Jakob disease; viral infection;  
XX gene therapy; mouse; expressed sequence tag; ds.

OS Homo sapiens.

XX WO200100643-A2.

XX 04-JAN-2001.

XX 19-JUN-2000; 2000WO-IL000358.

XX 25-JUN-1999; 99US-0140801P.

XX (INSI-) INSIGHT STRATEGY & MARKETING LTD.

XX Pecker I, Michal I, Itzhaki H;

XX WPI; 2001-137930/14.

PT New polynucleotides and polypeptides that are distantly homologous to  
PT heparanase, useful in wound healing, as well as in gene therapy protocols  
XX for angiogenesis, restenosis, atherosclerosis, or inflammation.

PS Example 1; Page 67; 67pp; English.

XX This sequence represents a human heparanase coding sequence clone,  
CC isolated from an EST clone. The invention relates to heparanase DNA and  
CC protein sequences. The heparanase DNA and protein sequences are useful in  
CC wound healing, angiogenesis, restenosis, atherosclerosis, inflammation,  
CC pulmonary diseases, neurodegenerative diseases (such as Scrape,  
CC Alzheimer's disease, and Creutzfeldt-Jakob disease) or viral infections.  
CC The heparanase coding sequence is particularly useful in gene therapy

XX  
SQ Sequence 1721 BP; 451 A; 413 C; 410 G; 447 T; 0 U; 0 Other;

Query Match	99.98	Score 1719.4	DB 4	Length 1721
Best Local Similarity	99.98	Pred. No. 0		
Matches 1720	Conservative 0	Mismatches 1	Indels 0	Gaps 0
Qy 1	CTAGAGCTTTTCGACTCTCCGTCGCGCGCAGCTGGCGGGGGAGCAGCCAGGTGAGCCCA	60		
Db 1	CTAGAGCTTTTCGACTCTCCGTCGCGCGCAGCTGGCGGGGGAGCAGCCAGGTGAGCCCA	60		
Qy 61	AGATGCTGCTCGCTCGAAGCTGCGCTGCGCGCGCGCTGATGCTGCTCTCTGGGC	120		
Db 61	AGATGCTGCTCGCTCGAAGCTGCGCTGCGCGCGCGCTGATGCTGCTCTCTGGGC	120		
Qy 121	CGCTGGGTCCTCTCCCTCGCGCGCTGCGCTGCGCGCGCTGCGCTGCTCTCTGGGC	180		
Db 121	CGCTGGGTCCTCTCCCTCGCGCGCTGCGCTGCGCGCGCTGCGCTGCTCTCTGGGC	180		
Qy 181	ACCTGGACTTTCTTCAACAGGAGCGCTGCACTGTGTGAGCCCTCGTCTCTGTCGTCA	240		
Db 181	ACCTGGACTTTCTTCAACAGGAGCGCTGCACTGTGTGAGCCCTCGTCTCTGTCGTCA	240		
Qy 241	CAATTGAGCGCAACTGCGCAGCGACCGCGGTTCTCATCTCTCGGGTTCTCCAAAGC	300		
Db 241	CAATTGAGCGCAACTGCGCAGCGACCGCGGTTCTCATCTCTCGGGTTCTCCAAAGC	300		
Qy 301	TTGCTACTTTGGCCAGAGGCTTGCTCTCGGTACCTGAGGTTTGGTGGCCAAAGACAG	360		
Db 301	TTGCTACTTTGGCCAGAGGCTTGCTCTCGGTACCTGAGGTTTGGTGGCCAAAGACAG	360		
Qy 361	ACTTCTCTAAATTTTCGATCCCAAGAGGAATCAACCTTTGAAGAGAGATTACTTGGCAAT	420		
Db 361	ACTTCTCTAAATTTTCGATCCCAAGAGGAATCAACCTTTGAAGAGAGATTACTTGGCAAT	420		
Qy 421	CTCAAGTCAACAGGATATTTGCAAAATATGGATCCATCCCTCTCTGATGTGGAGAGAGT	480		
Db 421	CTCAAGTCAACAGGATATTTGCAAAATATGGATCCATCCCTCTCTGATGTGGAGAGAGT	480		
Qy 481	TACGTTGGATGGCCCTACAGAGCAATTTGCTACTCCGAGACACTACAGAAAAGT	540		
Db 481	TACGTTGGATGGCCCTACAGAGCAATTTGCTACTCCGAGACACTACAGAAAAGT	540		
Qy 541	TCAAGAACAGCACCCTACTCAAGAGCTCTGTAGATGTGCTATACACTTTTGCACAACTGCT	600		
Db 541	TCAAGAACAGCACCCTACTCAAGAGCTCTGTAGATGTGCTATACACTTTTGCACAACTGCT	600		
Qy 601	CAGGACTGGAATTGATCTTTGGGCTAAATCGTTTATTAAGAACAGCAGATTTGCAGTGA	660		
Db 601	CAGGACTGGAATTGATCTTTGGGCTAAATCGTTTATTAAGAACAGCAGATTTGCAGTGA	660		
Qy 661	ACAGTTCTAATGCTCAGTTGCTCTGCTGACTACTGCTCTTCCAGGGGTATAAATTTCTT	720		
Db 661	ACAGTTCTAATGCTCAGTTGCTCTGCTGACTACTGCTCTTCCAGGGGTATAAATTTCTT	720		
Qy 721	GGGAACCTAGGCAATGAACCTAAAGTTTCTTAAAGAGGCTGATATTTTTCATCAATGGGT	780		
Db 721	GGGAACCTAGGCAATGAACCTAAAGTTTCTTAAAGAGGCTGATATTTTTCATCAATGGGT	780		
Qy 781	CGCAGTTAGGAGAGATTTTATTTCATTTGCATAAATCTTCTAAGAAAGTCCACCTTCAAAA	840		

## RESULT 6

ADG88801

ID ADG88801 standard; cDNA; 1721 BP.

XX

XX ADG88801;

XX AC

DT 11-MAR-2004 (first entry)

XX

DE Human hpa cDNA.

Db 781	CGCAGTTAGGAGAGATTTATTTCAATTCATAAACTTCTAAGAAAAGTCACCTTCAAAA	840
Qy 841	ATCAAAATCTATGCTCTGCTGATGTTGGTCAGCTCGAAGAAAAGCGCTAAGATGCTGA	900
Db 841	ATCAAAATCTATGCTCTGCTGATGTTGGTCAGCTCGAAGAAAAGCGCTAAGATGCTGA	900
Qy 901	AGAGCTTCTGAAAGGCTGTTGGAAGATGATTAATTCAGTTACATGTCATCTACTATT	960
Db 901	AGAGCTTCTGAAAGGCTGTTGGAAGATGATTAATTCAGTTACATGTCATCTACTATT	960
Qy 961	TGAATGAGCGGACTGCTACCGAGGAATTTTCTAAACCTTGATGTTGGACATTTTAA	1020
Db 961	TGAATGAGCGGACTGCTACCGAGGAATTTTCTAAACCTTGATGTTGGACATTTTAA	1020
Qy 1021	TTTTCATCTGTCAAAAAGTTTTCAGGTGTTTCAGAGCACCAGGCTTGGCAAGAGTCT	1080
Db 1021	TTTTCATCTGTCAAAAAGTTTTCAGGTGTTTCAGAGCACCAGGCTTGGCAAGAGTCT	1080
Qy 1081	GGTTAGGAGAAAACAAGCTCTGCATATGGAGCGGAGCGCCCTTGTCTATCCGACACCTTTG	1140
Db 1081	GGTTAGGAGAAAACAAGCTCTGCATATGGAGCGGAGCGCCCTTGTCTATCCGACACCTTTG	1140
Qy 1141	CAGCTGGCTTATGCTGGCTGGATAAATTTGGGCTGTGAGGCGGAGCGCCCTTGGGAATAGAAGTGG	1200
Db 1141	CAGCTGGCTTATGCTGGCTGGATAAATTTGGGCTGTGAGGCGGAGCGCCCTTGGGAATAGAAGTGG	1200
Qy 1201	TGATGAGGCAAGTATTTCTTTGGAGCAGGAAATACCATTTAGTGGATGAAAACCTTCCGATC	1260
Db 1201	TGATGAGGCAAGTATTTCTTTGGAGCAGGAAATACCATTTAGTGGATGAAAACCTTCCGATC	1260
Qy 1261	CTTTTACCTGATTTAGCTATCTCTCTGTTCAAGAAATTTGGTGGGACCAAGGTGTTAA	1320
Db 1261	CTTTTACCTGATTTAGCTATCTCTCTGTTCAAGAAATTTGGTGGGACCAAGGTGTTAA	1320
Qy 1321	TGGCAAGCTGCAAGGTTTCAAGAGAGAGGAGCTTCGAGTATACCTTCATTGACACAAACA	1380
Db 1321	TGGCAAGCTGCAAGGTTTCAAGAGAGAGGAGCTTCGAGTATACCTTCATTGACACAAACA	1380
Qy 1381	CTGCAATCAAGGTATTAAGAGAGGAGATTTAACTCTGTATGCTATAAACCCTCCATAACG	1440
Db 1381	CTGCAATCAAGGTATTAAGAGAGGAGATTTAACTCTGTATGCTATAAACCCTCCATAACG	1440
Qy 1441	TCACCAAGTACTTTGCGGTTTACCCCTATCCCTTTTCTAACCAAGCAAGTGGATAACCTTC	1500
Db 1441	TCACCAAGTACTTTGCGGTTTACCCCTATCCCTTTTCTAACCAAGCAAGTGGATAACCTTC	1500
Qy 1501	TAAAGCTTTGGGACCTCATGATTTACTTCCAAATCTGTCCAACTCAATGGTCTAACTC	1560
Db 1501	TAAAGCTTTGGGACCTCATGATTTACTTCCAAATCTGTCCAACTCAATGGTCTAACTC	1560
Qy 1561	TAAAGATGTTGGATGATCAAACTTCCACCTTTTAAATGAAAACCTCTCCGCGCCAGGAA	1620
Db 1561	TAAAGATGTTGGATGATCAAACTTCCACCTTTTAAATGAAAACCTCTCTCCGCGCCAGGAA	1620
Qy 1621	GTTTCACTGGGCTTGGCAGGCTTTCTCATATAGTTTTTTTGTGATAAGAAATGCCAAAGTTG	1680
Db 1621	GTTTCACTGGGCTTGGCAGGCTTTCTCATATAGTTTTTTTGTGATAAGAAATGCCAAAGTTG	1680
Qy 1681	CTGCTTGCATCTGAAAATAAATAATATAGTCTCTGACACTG 1721	
Db 1681	CTGCTTGCATCTGAAAATAAATAATATAGTCTCTGACACTG 1721	

## RESULT 6

ADG88801

ID ADG88801 standard; cDNA; 1721 BP.

XX

XX ADG88801;

XX AC

DT 11-MAR-2004 (first entry)

XX

DE Human hpa cDNA.



XX Wound healing; heparanase; ulcer; burn; laceration; surgical incision;  
 KW necrosis; pressure wound; diabetic ulcer; angiogenesis; human; therapy;  
 KW gene; ss.

XX Homo sapiens.

XX OS Location/Qualifiers  
 XX FH 63. .1694  
 XX FT /\*tag= a  
 XX FT /product= "Human hpa protein"

XX PN US2003161823-A1.

XX PD 28-AUG-2003.

XX PF 14-JAN-2003; 2003US-00341582.

XX PR 31-AUG-1998; 98WO-US017954.

XX PR 01-MAR-1999; 99US-00258892.

XX PR 06-FEB-2001; 2001US-00776874.

XX PR 05-SEP-2001; 2001US-IL000830.

XX PR 19-NOV-2001; 2001US-00988113.

XX PA (ILAN/) ILAN N.

XX PA (VLOD/) VLODAVSKY I.

XX PA (YACO/) YACOBY-ZEEVI O.

XX PA (PECK/) PECKER I.

XX PA (FEIN/) FEINSTEIN E.

XX PI Ilan N, Vlodaysky I, Yacoby-Zeevi O, Pecker I, Feinstein E;  
 XX DR WPI; 2003-897910/82.

XX DR P-PSDB; ADG88800.

XX PT Composition for treating a wound comprising recombinant heparanase is  
 XX PT useful to induce or accelerate wound healing and induce or accelerate  
 XX PT angiogenesis.

XX PS Example 1; SEQ ID NO 11; 143pp; English.

XX CC The present invention relates to methods and compositions for inducing  
 XX CC and/or accelerating wound healing via the catalytic activity of  
 XX CC heparanase. The invention is used to induce or accelerate a healing  
 XX CC process, particularly of an ulcer, burn, laceration, surgical incision,  
 XX CC necrosis, pressure wound, diabetic ulcer and to induce or accelerate  
 XX CC angiogenesis. The present sequence is human hpa cDNA.

XX SQ Sequence 1721 BP; 451 A; 413 C; 410 G; 447 T; 0 U; 0 Other;

Query Match 99.9%; Score 1719.4; DB 10; Length 1721;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 1720; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTAGAGCTTTCCGACTCTCCGCTGCGCGGAGCTGCGGGGGGAGCAGCAGGTGAGCCCA 60

DB 1 CTAGAGCTTTCCGACTCTCCGCTGCGCGGAGCTGCGGGGGGAGCAGCAGGTGAGCCCA 60

QY 61 AGATGCTGCTGCTCGAAGCTCGCTGCGCGCGCGCGCTGATGCTGCTCTCGGGC 120

DB 61 AGATGCTGCTGCTCGAAGCTCGCTGCGCGCGCGCGCTGATGCTGCTCTCGGGC 120

QY 121 CGCTGGGTCCCTCTCCCTGGCGCCCTGCCCGACCTGGCGAAGCAGAGCTCGTG 180

DB 121 CGCTGGGTCCCTCTCCCTGGCGCCCTGCCCGACCTGGCGAAGCAGAGCTCGTG 180

QY 181 ACCTGGAGCTCTTCCACCAGAGCGCTGCACTGCTGGTGGCCCTCTGCTGCTGCA 240

DB 181 ACCTGGAGCTCTTCCACCAGAGCGCTGCACTGCTGGTGGCCCTCTGCTGCTGCA 240

QY 241 CCATTGACGCCAACCTGGCCACGACCGCGGGTTCTCATCTCTCGGGTTCTCCAAAGC 300

DB 241 CCATTGACGCCAACCTGGCCACGACCGCGGGTTCTCATCTCTCGGGTTCTCCAAAGC 300

301 TTCTGTACCTTTGGCCAGAGGCTTGTCTCTCGGTACCTGAGGTTTGGTGGCACCAGACAG 360

DB 301 TTCTGTACCTTTGGCCAGAGGCTTGTCTCTCGGTACCTGAGGTTTGGTGGCACCAGACAG 360

QY 361 ACTTCCTAAATTTTCGATCCCAAGAGGAATCAACCTTTTGAAGAGAGAAAGTTACTTGGCAAT 420

DB 361 ACTTCCTAAATTTTCGATCCCAAGAGGAATCAACCTTTTGAAGAGAGAAAGTTACTTGGCAAT 420

QY 421 CTCAAGTCAACACGAGATATTTTGCAAAATATGGATCCATCCCTCTGATGTGGAGGAGAAGT 480

DB 421 CTCAAGTCAACACGAGATATTTTGCAAAATATGGATCCATCCCTCTGATGTGGAGGAGAAGT 480

QY 481 TAGGTTTGGAAATGGCCCTACAGAGCAATTTGCTACTCCGAGAACACTACAGAAAAAGT 540

DB 481 TAGGTTTGGAAATGGCCCTACAGAGCAATTTGCTACTCCGAGAACACTACAGAAAAAGT 540

QY 541 TCAAGAACAGACCTACTCAAGAAAGCTCTAGATGTGCTATACACTTTTGCAAACTGCT 600

DB 541 TCAAGAACAGACCTACTCAAGAAAGCTCTAGATGTGCTATACACTTTTGCAAACTGCT 600

QY 601 CAGGACTGGACTTGATCTTTGGGCTAAATCGGTTATTAAGAACAGACAGATTTGCAAGTGA 660

DB 601 CAGGACTGGACTTGATCTTTGGGCTAAATCGGTTATTAAGAACAGACAGATTTGCAAGTGA 660

QY 661 ACAGTTCTAATGCTCAGTTGCTCTCGACTACTGCTCTCCAGGGGTATTAACATTTCTT 720

DB 661 ACAGTTCTAATGCTCAGTTGCTCTCGACTACTGCTCTCCAGGGGTATTAACATTTCTT 720

QY 721 GGGAACTAGGCAATGAACCTAAACAGATTTTCCCTAAGAAAGGCTGATATTTTCAATCAATGGGT 780

DB 721 GGGAACTAGGCAATGAACCTAAACAGATTTTCCCTAAGAAAGGCTGATATTTTCAATCAATGGGT 780

QY 781 CGCAGTTAGGAGAAAGATTTTATTCAAATTCGATATAAATCTTAAAGAAAGTCCACCTTCAAAA 840

DB 781 CGCAGTTAGGAGAAAGATTTTATTCAAATTCGATATAAATCTTAAAGAAAGTCCACCTTCAAAA 840

QY 841 ATGCAAAACTCTATGCTCTGATGTTGGTCCAGCTCGAAGAAAGACGGCTGAAGTCTGA 900

DB 841 ATGCAAAACTCTATGCTCTGATGTTGGTCCAGCTCGAAGAAAGACGGCTGAAGTCTGA 900

QY 901 AGAGCTTCCTGAAGGCTGGTGGAGAGTGAATGATTCAGTTACATGGCATTACACTACTATT 960

DB 901 AGAGCTTCCTGAAGGCTGGTGGAGAGTGAATGATTCAGTTACATGGCATTACACTACTATT 960

QY 961 TGAATGGACGGACTGCTTACAGGGAAGATTTCTAAACCTGATGATTAAGCAATTTTAA 1020

DB 961 TGAATGGACGGACTGCTTACAGGGAAGATTTCTAAACCTGATGATTAAGCAATTTTAA 1020

QY 1021 TTTTCATCTGTGCAAAAAGTTTTCAGGTGGTTGAGAGCACCGGCTGGCAAGAGGCTCT 1080

DB 1021 TTTTCATCTGTGCAAAAAGTTTTCAGGTGGTTGAGAGCACCGGCTGGCAAGAGGCTCT 1080

QY 1081 GGTTAGGAGAAAAAAGCTCTGCAATATGGAGCGGAGCGGCTTGTCTATCCGACACCTTTG 1140

DB 1081 GGTTAGGAGAAAAAAGCTCTGCAATATGGAGCGGAGCGGCTTGTCTATCCGACACCTTTG 1140

QY 1141 CAGCTGGCTTTTATGTGGCTGGATAAATTTGGGCTGTGAGCCCGAATGGGAATAGAAGTGG 1200

DB 1141 CAGCTGGCTTTTATGTGGCTGGATAAATTTGGGCTGTGAGCCCGAATGGGAATAGAAGTGG 1200

QY 1201 TGATGGGCAAGTATTTCTTTGGAGCAGGAACCTACCAATTTAGTGGATGAAAACCTTCGATC 1260

DB 1201 TGATGGGCAAGTATTTCTTTGGAGCAGGAACCTACCAATTTAGTGGATGAAAACCTTCGATC 1260

QY 1261 CTTTACCTGATTTATGGCTATCTCTTCTGTTCAGAAATTTGGTGGGCAACAAGGTGTAA 1320

DB 1261 CTTTACCTGATTTATGGCTATCTCTTCTGTTCAGAAATTTGGTGGGCAACAAGGTGTAA 1320

QY 1321 TGGCAAGCGTGCAGGTTTCAAGAGAGGAAGTTCGAGTATACCTTTTATTCGCAAAAACA 1380

DB 1321 TGGCAAGCGTGCAGGTTTCAAGAGAGGAAGTTCGAGTATACCTTTTATTCGCAAAAACA 1380





Db 841 ATGCAAACTCTATGTCCTGATGTTGGTCAGCCCTCGAAGAAAGACGCTAAGATGCTGA 900  
Qy 901 AGAGCTTCCTGAAGCTGGTGGAGAGTGATTGATTCAGTTACATGGCATCACTACTATT 960  
Db 901 AGAGCTTCCTGAAGCTGGTGGAGAGTGATTGATTCAGTTACATGGCATCACTACTATT 960  
Qy 961 TGAATGGACGAGCTGCTACACGAGGAAGATTTCCTAAACCCCTGATGTATTGGACATTTTTA 1020  
Db 961 TGAATGGACGAGCTGCTACACGAGGAAGATTTCCTAAACCCCTGATGTATTGGACATTTTTA 1020  
Qy 1021 TTTCACTGTGCAAAAAGTTTTCCAGGTGGTTGAGAGCACCAAGCCCTGGCAAGAGTCT 1080  
Db 1021 TTTCACTGTGCAAAAAGTTTTCCAGGTGGTTGAGAGCACCAAGCCCTGGCAAGAGTCT 1080  
Qy 1081 GGTTAGGAGAACAGCTCTGCATATGGAGGGGAGCGCCCTTCTATCCGACACCTTTG 1140  
Db 1081 GGTTAGGAGAACAGCTCTGCATATGGAGGGGAGCGCCCTTCTATCCGACACCTTTG 1140  
Qy 1141 CAGCTGGCTTTATGTGGCTGATATAATTTGGCCCTGTAGCCCGAATGGGAATAGAAGTGG 1200  
Db 1141 CAGCTGGCTTTATGTGGCTGATATAATTTGGCCCTGTAGCCCGAATGGGAATAGAAGTGG 1200  
Qy 1201 TGATGAGCAAGTATTTCTTTGGAGCAGGAACCTACCAATTTAGTGGATGAACCTTCGATC 1260  
Db 1201 TGATGAGCAAGTATTTCTTTGGAGCAGGAACCTACCAATTTAGTGGATGAACCTTCGATC 1260  
Qy 1261 CTTTACCTGATTATGCTATCTCTCTGTTCAAGAAATTTGGTGGGACCAAGGTGTAA 1320  
Db 1261 CTTTACCTGATTATGCTATCTCTCTGTTCAAGAAATTTGGTGGGACCAAGGTGTAA 1320  
Qy 1321 TGGCAAGCGTCAAGGTTCAAGAGAGAGGAGTTCGAGTATACCTTCATTGTCACAAACA 1380  
Db 1321 TGGCAAGCGTCAAGGTTCAAGAGAGAGGAGTTCGAGTATACCTTCATTGTCACAAACA 1380  
Qy 1381 CTGCAATCCAGGTATATAAGAGAGGATTTTAACTCTGTATGCCATAAACCTCCATAACG 1440  
Db 1381 CTGCAATCCAGGTATATAAGAGAGGATTTTAACTCTGTATGCCATAAACCTCCATAACG 1440  
Qy 1441 TCACCAAGTACTTGGGTACCCCTATCCTTTTCTTAACAAGCAAGTGATTAATACCTTC 1500  
Db 1441 TCACCAAGTACTTGGGTACCCCTATCCTTTTCTTAACAAGCAAGTGATTAATACCTTC 1500  
Qy 1501 TAAGACCTTTGGGACCTCATGGATTACTTTTCCAAATCTGTCCAACCTCAATGGTCTAACTC 1560  
Db 1501 TAAGACCTTTGGGACCTCATGGATTACTTTTCCAAATCTGTCCAACCTCAATGGTCTAACTC 1560  
Qy 1561 TAAAGATGGTGGATGATCAAAACCTTGGCACCTTTTAAATGGAAAAACCTTCGCGCCAGGAA 1620  
Db 1561 TAAAGATGGTGGATGATCAAAACCTTGGCACCTTTTAAATGGAAAAACCTTCGCGCCAGGAA 1620  
Qy 1621 GTTCACTGGGCTTGGCAGCTTCTCATATAGTTTTTTTGTGATAAGAAATGCCAAAGTTG 1680  
Db 1621 GTTCACTGGGCTTGGCAGCTTCTCATATAGTTTTTTTGTGATAAGAAATGCCAAAGTTG 1680  
Qy 1681 CTGCTTGATCTGAAAAATAAATAATACTAGTCCCTGACACTG 1721  
Db 1681 CTGCTTGATCTGAAAAATAAATAATACTAGTCCCTGACACTG 1721

RESULT 8

ID ADL16380 standard; cDNA; 1721 BP.

XX ADL16380;

AC ADL16380 (first entry)

DT 06-MAY-2004 Human heparanase partial cDNA #2.

DE Human; ss; heparanase; gene; heparanase-dependent cancer; cancer;  
KW autoimmune reaction; inflammation; chromosome 4.  
XX Homo sapiens.

XX US2003236215-A1.  
PN 25-DEC-2003.  
XX 09-JUN-2003; 2003US-00456573.  
XX 31-AUG-1998; 98WO-US017954.  
PR 01-MAR-1999; 99US-00258892.  
PR 08-NOV-1999; 99US-00435739.  
XX (INSI-) INSIGHT STRATEGY & MARKETING LTD.  
PA (HADA-) HADASIT MEDICAL RES SERVICES & DEV.  
XX Pecker I, Vlodavsky I, Feinstein E;  
XX WPI; 2004-070610/07.  
XX New antisense oligonucleotide hybridizable with a polynucleotide encoding  
PT a polypeptide with heparanase activity, useful for treating diseases such  
PT as cancer and autoimmune disorders.  
XX Example 1; SEQ ID NO 11; 108pp; English.  
XX The invention relates to an antisense oligonucleotide (ASO) comprising a  
CC polynucleotide or a polynucleotide analogue of at least 10 bases being  
CC hybridisable in vivo, under physiological conditions, with a portion of  
CC a polynucleotide strand encoding a polypeptide having heparanase  
CC catalytic activity. Also included are a method of in vivo downregulating  
CC heparanase activity (comprising administering the ASO in vivo), a method  
CC of treating a subject suffering from a pathological condition  
CC (characterised by heparanase activity, comprising administering ASO to  
CC the subject), a pharmaceutical composition comprising the ASO and a  
CC carrier, an antisense nucleic acid construct (comprising a promoter  
CC sequence and a polynucleotide sequence directing the synthesis of an  
CC antisense RNA sequence of at least 10 bases being hybridisable in vivo,  
CC under physiological conditions, with a polynucleotide strand encoding a  
CC polypeptide having heparanase catalytic activity), a method of in vivo  
CC downregulating heparanase activity (comprising administering in vivo the  
CC antisense nucleic acid construct), a pharmaceutical composition  
CC comprising the antisense nucleic acid construct and a carrier, and an  
CC antisense oligonucleotide comprising a polynucleotide or a polynucleotide  
CC analogue of at least 10 bases being hybridisable in vivo, under  
CC physiological conditions, with a portion of a polynucleotide strand being  
CC characterised by forming at least a portion of an untranslated region  
CC (UTR) for a polynucleotide strand encoding a polypeptide having  
CC heparanase catalytic activity. The methods and compositions of the  
CC present invention are useful for the prevention and/or treatment of  
CC diseases or conditions associated with aberrant heparanase activity, such  
CC as heparanase-dependent cancer, cancer, autoimmune reaction and  
CC inflammation. The gene for human heparanase is located on chromosome 4.  
CC The present sequence is a human heparanase cDNA.  
XX Sequence 1721 BP; 451 A; 413 C; 410 G; 447 T; 0 U; 0 Other;

Query Match 99.9%; Score 1719.4; DB 12; Length 1721;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1720; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CTAGAGCTTTTCGACTCTCCGCTGCGGCGAGCTGGCGGGGGAGCAGCAGGTGAGCCCA 60  
Db 1 CTAGAGCTTTTCGACTCTCCGCTGCGGCGAGCTGGCGGGGGAGCAGCAGGTGAGCCCA 60  
Qy 61 AGATGCTGCTGCGCTCGAAGCCTGCGCTGCGCGCGCGCTGATGCTGCTCTCTCTGGGC 120  
Db 61 AGATGCTGCTGCGCTCGAAGCCTGCGCTGCGCGCGCGCTGATGCTGCTCTCTCTGGGC 120  
Qy 121 CGCTGGGTCCCTCTCCCTGGCGCCTGCCGACCTGCGGAGCAGACAGACGTCTGTGG 180  
Db 121 CGCTGGGTCCCTCTCTCCCTGGCGCCTGCCGACCTGCGGAGCAGACAGACGTCTGTGG 180  
Qy 181 ACCTGGACTTCTTTCACCCAGGAGCGCTGCACCTGGTGAAGCCCTCGTCTGTCTCGTCA 240

Db 181 ACCTGGAATCTTCCACCCAGAGCCGCTGCACCTGGTGAGCCCTCCTGTTCTGTCCTGCA 240  
Qy 241 CCATTGACGCAACTGCGCACGACCGCGGGTTCCTCATCTCCTCGGGTTCCTCAAAGC 300  
Db 241 CCATTGACGCAACTGCGCACGACCGCGGGTTCCTCATCTCCTCGGGTTCCTCAAAGC 300  
Qy 301 TTCGTACTTGGCCAGAGGCTTGCTCCTCGGTACCTGAGCTTGGTGGCAACCAAGACAG 360  
Db 301 TTCGTACTTGGCCAGAGGCTTGCTCCTCGGTACCTGAGCTTGGTGGCAACCAAGACAG 360  
Qy 361 ACTTCTTAATTTTCGATCCCAAGAGGAATCAACCTTTGAAGAGAGTACTGCGCAAT 420  
Db 361 ACTTCTTAATTTTCGATCCCAAGAGGAATCAACCTTTGAAGAGAGTACTGCGCAAT 420  
Qy 421 CTCAGTCAACACGAGATTTGCAATATGATCCATCCCTCCTGATGTGGAGGAGAAGT 480  
Db 421 CTCAGTCAACACGAGATTTGCAATATGATCCATCCCTCCTGATGTGGAGGAGAAGT 480  
Qy 481 TAGCGTTGGAATGSCCTACAGAGCAATTTGCTACTCCGAGAACACTACAGAAAAAGT 540  
Db 481 TAGCGTTGGAATGSCCTACAGAGCAATTTGCTACTCCGAGAACACTACAGAAAAAGT 540  
Qy 541 TCAGAACACGACCTACTCAAGAGCTCTGTAGATGTCTATACACTTTTGCACACTGCT 600  
Db 541 TCAGAACACGACCTACTCAAGAGCTCTGTAGATGTCTATACACTTTTGCACACTGCT 600  
Qy 601 CAGGACTGGACTTGATCTTTGGCCCTAAATGCTTTAAGAACAGCAGATTTGCAAGTGA 660  
Db 601 CAGGACTGGACTTGATCTTTGGCCCTAAATGCTTTAAGAACAGCAGATTTGCAAGTGA 660  
Qy 661 ACAGTTCTAATGTCTGCTGCTGACTACTGCTCTTCCAGGGGTATAACATTTCTT 720  
Db 661 ACAGTTCTAATGTCTGCTGCTGACTACTGCTCTTCCAGGGGTATAACATTTCTT 720  
Qy 721 GGGAACTAGGCAATGAACCTAACAGTTTCCCTTAAGAAAGGCTGATATTTTCAATGGGT 780  
Db 721 GGGAACTAGGCAATGAACCTAACAGTTTCCCTTAAGAAAGGCTGATATTTTCAATGGGT 780  
Qy 781 CGCAGTTAGGAGAGATTTTATTCATTAATGATTAACCTTCAAGAAAGTCCACCTTCAAAA 840  
Db 781 CGCAGTTAGGAGAGATTTATTCATTAATGATTAACCTTCAAGAAAGTCCACCTTCAAAA 840  
Qy 841 ATGCAAACTCTATGCTCTGATGTTGGTTCAGCCTCGAAGAAAGACGGCTTAAGATGCTGA 900  
Db 841 ATGCAAACTCTATGCTCTGATGTTGGTTCAGCCTCGAAGAAAGACGGCTTAAGATGCTGA 900  
Qy 901 AGAGCTTCTGAAGGCTGGTGGAGAGTGTGATTCAGTTACATGCGATCACTACTATT 960  
Db 901 AGAGCTTCTGAAGGCTGGTGGAGAGTGTGATTCAGTTACATGCGATCACTACTATT 960  
Qy 961 TGAATGACGAGCTGTACAGGGAAGATTTTCTAAACCTGTATGATGACATTTTAA 1020  
Db 961 TGAATGACGAGCTGTACAGGGAAGATTTTCTAAACCTGTATGATGACATTTTAA 1020  
Qy 1021 TTTTCATCTGCAAAAAGTTTCCAGGTGTTGAGAGCACCGCCCTGGCAAGAGTCT 1080  
Db 1021 TTTTCATCTGCAAAAAGTTTCCAGGTGTTGAGAGCACCGCCCTGGCAAGAGTCT 1080  
Qy 1081 GGTAGAGAAAACAGCTCTGCATATGAGGCGGAGGCGCTTCTATCCGACACCTTTG 1140  
Db 1081 GGTAGAGAAAACAGCTCTGCATATGAGGCGGAGGCGCTTCTATCCGACACCTTTG 1140  
Qy 1141 CAGCTGCTTTATGTGCTGATAAATTTGGSCCTGTGAGCCGCAATGGGAATGAGTGG 1200  
Db 1141 CAGCTGCTTTATGTGCTGATAAATTTGGSCCTGTGAGCCGCAATGGGAATGAGTGG 1200  
Qy 1201 TGATGAGCAAGTATTTCTTGGAGCAGGAACTACCAATTTAGTGGATGAAAACCTTCGATC 1260  
Db 1201 TGATGAGCAAGTATTTCTTGGAGCAGGAACTACCAATTTAGTGGATGAAAACCTTCGATC 1260  
Qy 1261 CTTTACCTGATATTGCGTATCTCTTCTGTTCAAGAAATTTGGTGGGCAACCAAGGTGTTAA 1320  
Db 1261 CTTTACCTGATATTGCGTATCTCTTCTGTTCAAGAAATTTGGTGGGCAACCAAGGTGTTAA 1320

Qy 1321 TGGCAAGCGTGCAGGTTCAAAGAGAGGAGCTTCGAGTATACCTTTCAATTCGACAAACA 1380  
Db 1321 TGGCAAGCGTGCAGGTTCAAAGAGAGGAGCTTCGAGTATACCTTTCAATTCGACAAACA 1380  
Qy 1381 CTGACAATCAAGGTATAAAGAGGAGATTAACTCTGTATGCGATAAACCTCCATTAACG 1440  
Db 1381 CTGACAATCAAGGTATAAAGAGGAGATTAACTCTGTATGCGATAAACCTCCATTAACG 1440  
Qy 1441 TCACCAAGTACTTGGCGTTACCTATCTCTTTTCTAACAGAGAGTGGATAAATACCTTC 1500  
Db 1441 TCACCAAGTACTTGGCGTTACCTATCTCTTTTCTAACAGAGAGTGGATAAATACCTTC 1500  
Qy 1501 TAAGACCTTTGGGACCTCATGGAATATTTTCCAAATCTGTCCAACTCAATGGTCTAACTC 1560  
Db 1501 TAAGACCTTTGGGACCTCATGGAATATTTTCCAAATCTGTCCAACTCAATGGTCTAACTC 1560  
Qy 1561 TAAAGATGTGGATGATCAAACTTGGCACCTTTAATGGAAAAACCTCTCCGGCCAGGAA 1620  
Db 1561 TAAAGATGTGGATGATCAAACTTGGCACCTTTAATGGAAAAACCTCTCCGGCCAGGAA 1620  
Qy 1621 GTTCACTGGGCTTGGCAGCTTCTCATATAGTTTTTTTGTGATAAGAAATGCCAAAGTTG 1680  
Db 1621 GTTCACTGGGCTTGGCAGCTTCTCATATAGTTTTTTTGTGATAAGAAATGCCAAAGTTG 1680  
Qy 1681 CTGCTTGCATCTGAAAATAAATAATATATAGTCTCCTGACACTG 1721  
Db 1681 CTGCTTGCATCTGAAAATAAATAATATATAGTCTCCTGACACTG 1721

## RESULT 9

ADL16378

ID ADL16378 standard; cDNA; 1721 BP.

XX

AC ADL16378;

XX

DT 06-MAY-2004 (first entry)

XX

XX Human heparanase partial cDNA #1.

XX

XX Human; ss; heparanase; gene; heparanase-dependent cancer; cancer;  
KW autoimmune reaction; inflammation; chromosome 4.

XX

XX Homo sapiens.

XX

XX Key Location/Qualifiers

XX 3'UTR 1695..1721

XX FT /\*tag= a

XX FT /note= "Claimed in claim 20"

XX

XX US2003236215-A1.

XX

XX 25-DEC-2003.

XX

XX 09-JUN-2003; 2003US-00456573.

XX

XX 31-AUG-1998; 98WO-US017954.

XX

XX 01-MAR-1999; 99US-00258892.

XX

XX 08-NOV-1999; 99US-00435739.

XX

XX (INSI-) INSIGHT STRATEGY &amp; MARKETING LTD.

XX

XX (HADA-) HADASIT MEDICAL RES SERVICES &amp; DEV.

XX

XX Pecker I, Vlodavsky I, Feinstein E;

XX

XX WPI; 2004-070610/07.

XX

XX New antisense oligonucleotide hybridizable with a polynucleotide encoding

XX a polypeptide with heparanase activity, useful for treating diseases such

XX as cancer and autoimmune disorders.

XX

XX Claim 2; SEQ ID NO 9; 108pp; English.

XX

CC The invention relates to an antisense oligonucleotide (ASO) comprising a  
 CC polynucleotide or a polynucleotide analogue of at least 10 bases being  
 CC hybridisable *in vivo*, under physiological conditions, with a portion of  
 CC a polynucleotide strand encoding a polypeptide having heparanase  
 CC catalytic activity. Also included are a method of *in vivo* downregulating  
 CC heparanase activity (comprising administering the ASO *in vivo*), a method  
 CC of treating a subject suffering from a pathological condition  
 CC (characterised by heparanase activity, comprising administering ASO to  
 CC the subject), a pharmaceutical composition comprising the ASO and a  
 CC carrier, an antisense nucleic acid construct (comprising a promoter  
 CC sequence and a polynucleotide sequence directing the synthesis of an  
 CC antisense RNA sequence of at least 10 bases being hybridisable *in vivo*,  
 CC under physiological conditions, with a polynucleotide strand encoding a  
 CC polypeptide having heparanase catalytic activity), a method of *in vivo*  
 CC downregulating heparanase activity (comprising administering *in vivo* the  
 CC antisense nucleic acid construct), a pharmaceutical composition  
 CC comprising the antisense nucleic acid construct and a carrier, and an  
 CC antisense oligonucleotide comprising a polynucleotide or a polynucleotide  
 CC analogue of at least 10 bases being hybridisable *in vivo*, under  
 CC physiological conditions, with a portion of a polynucleotide strand being  
 CC characterised by forming at least a portion of an untranslated region  
 CC (UTR) for a polynucleotide strand encoding a polypeptide having  
 CC heparanase catalytic activity. The methods and compositions of the  
 CC present invention are useful for the prevention and/or treatment of  
 CC diseases or conditions associated with aberrant heparanase activity, such  
 CC as heparanase-dependent cancer, cancer, autoimmune reaction and  
 CC inflammation. The gene for human heparanase is located on chromosome 4.  
 CC The present sequence is a human heparanase cDNA.  
 XX  
 SQ

Query Match 99.9%; Score 1719.4; DB 12; Length 1721;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 1720; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	1	CTAGAGCTTTTCGACTCTCCGCTGGCGGCGACGCTGGCGGGGGAGCAGCAGGTGAGCCCA	60
Db	1	CTAGAGCTTTTCGACTCTCCGCTGGCGGCGACGCTGGCGGGGGAGCAGCAGGTGAGCCCA	60
Qy	61	AGATGCTGCTCGCTCGAAGCTCGGCTGGCGCGCGCGCTGATGCTGCTCTCTGGGGC	120
Db	61	AGATGCTGCTCGCTCGAAGCTCGGCTGGCGCGCGCGCTGATGCTGCTCTCTGGGGC	120
Qy	121	CGCTGGGTCCCTCTCCCTGGCGCCCTGCGCCGCGCGCTGATGCTGCTCTCTGGGGC	180
Db	121	CGCTGGGTCCCTCTCCCTGGCGCCCTGCGCCGCGCGCTGATGCTGCTCTCTGGGGC	180
Qy	181	ACCTGGACTTCTTCAACCAGAGCGCGTGCAACCTGGTGAGCCCTCGTTCTGTCCTGCA	240
Db	181	ACCTGGACTTCTTCAACCAGAGCGCGTGCAACCTGGTGAGCCCTCGTTCTGTCCTGCA	240
Qy	241	CCATTGACGCCAACTGGCCACGGAACCGCGGGTCTCATCTCTCTGGGTTCTCCAAAGC	300
Db	241	CCATTGACGCCAACTGGCCACGGAACCGCGGGTCTCATCTCTCTGGGTTCTCCAAAGC	300
Qy	301	TTCTGTACCTTGGCAGAGGCTTGCTCTGGGTACCTGAGGTTGGTGCCACCAAGACAG	360
Db	301	TTCTGTACCTTGGCAGAGGCTTGCTCTGGGTACCTGAGGTTGGTGCCACCAAGACAG	360
Qy	361	ACTTCTCTAAATTTTCGATCCCAAGAGGAATCAACCTTTGAAGAGAGAAGTTACTTGGCAAT	420
Db	361	ACTTCTCTAAATTTTCGATCCCAAGAGGAATCAACCTTTGAAGAGAGAAGTTACTTGGCAAT	420
Qy	421	CTCAAGTCAACAGGATATTTGCAAAATATGATGCATCCCTCTCTGATGTGGAGAGAAGT	480
Db	421	CTCAAGTCAACAGGATATTTGCAAAATATGATGCATCCCTCTCTGATGTGGAGAGAAGT	480
Qy	481	TACGGTGGAAATGSCCTTACCAGAGGCAATTTGCTACTCCGAGACACTTACCAGAAAAGT	540
Db	481	TACGGTGGAAATGSCCTTACCAGAGGCAATTTGCTACTCCGAGACACTTACCAGAAAAGT	540
Qy	541	TCAAGAACAGCACCTTACTCAAGAAAGCTCTGTAGATGTGCTATACACTTTTTCGAAACTGCT	600
Db			

Db	541	TCAAGAACAGCACCTACTCAAGAAAGCTCTCTAGATGTGCTATACACTTTTTCGAAACTGCT	600
Qy	601	CAGGACTGGACTTGATCTTTGGGCTTAATCGCTTATTAAGAACAGCAGAGATTGCGAGTGA	660
Db	601	CAGGACTGGACTTGATCTTTGGGCTTAATCGCTTATTAAGAACAGCAGAGATTGCGAGTGA	660
Qy	661	ACAGTTCTAATGTCTCAGTGTCTCTCGGACTACTGCTCTTCCAAAGGGGTATAAACATTTCTT	720
Db	661	ACAGTTCTAATGTCTCAGTGTCTCTCGGACTACTGCTCTTCCAAAGGGGTATAAACATTTCTT	720
Qy	721	GGGAACCTAGGCAATGAACCTAAACAGTTTCTTAAAGAGGCTGATATTTTTCATCAATCGGT	780
Db	721	GGGAACCTAGGCAATGAACCTAAACAGTTTCTTAAAGAGGCTGATATTTTTCATCAATCGGT	780
Qy	781	CGCAGTTTAGGAGAAGATTTTATTCATTTGATGATAAACTTCTAAGAAAGTCCACCTTCAAAA	840
Db	781	CGCAGTTTAGGAGAAGATTTTATTCATTTGATGATAAACTTCTAAGAAAGTCCACCTTCAAAA	840
Qy	841	ATGCAAAACTCTATGGTCTCTGATGTTGGTCAGGCTCGAAGAAAGACGGCTAAGATGCTGA	900
Db	841	ATGCAAAACTCTATGGTCTCTGATGTTGGTCAGGCTCGAAGAAAGACGGCTAAGATGCTGA	900
Qy	901	AGAGCTTCTGAAGGCTGGTGGAGAAAGTGAATGATTGATTCAGTTATCATGGCATCACTACTATT	960
Db	901	AGAGCTTCTGAAGGCTGGTGGAGAAAGTGAATGATTGATTCAGTTATCATGGCATCACTACTATT	960
Qy	961	TGAATGACACGAGCTGTACCCAGGGAGAATTTTCTTAAACCTCTGATGTATTTGACATTTTAA	1020
Db	961	TGAATGACACGAGCTGTACCCAGGGAGAATTTTCTTAAACCTCTGATGTATTTGACATTTTAA	1020
Qy	1021	TTTTCATCTGTGCAAAAAGTTTTCAGGTGGTTCAGAGCACACAGGCTTGGCAAGAGTCT	1080
Db	1021	TTTTCATCTGTGCAAAAAGTTTTCAGGTGGTTCAGAGCACACAGGCTTGGCAAGAGTCT	1080
Qy	1081	GGTTAGGAGAAAACAAGCTCTGCATATGAGAGCGGAGCGCCCTTGTCTATCCGACACCTTTG	1140
Db	1081	GGTTAGGAGAAAACAAGCTCTGCATATGAGAGCGGAGCGCCCTTGTCTATCCGACACCTTTG	1140
Qy	1141	CAGCTGGCTTTATGTGGCTGGATAAATTTGGGCTGTGAGCCCGAATGGGAATAGAAAGTGG	1200
Db	1141	CAGCTGGCTTTATGTGGCTGGATAAATTTGGGCTGTGAGCCCGAATGGGAATAGAAAGTGG	1200
Qy	1201	TGATGAGGCAAGTATTCTTTGGAGCAGAAACTACCAATTTAGTGGATGAAAACCTTCGATC	1260
Db	1201	TGATGAGGCAAGTATTCTTTGGAGCAGAAACTACCAATTTAGTGGATGAAAACCTTCGATC	1260
Qy	1261	CTTTACCTGATTTATGGCTATCTCTTCTGTTCAAGAAATTTGGTGGGCACCAAGGTGTAA	1320
Db	1261	CTTTACCTGATTTATGGCTATCTCTTCTGTTCAAGAAATTTGGTGGGCACCAAGGTGTAA	1320
Qy	1321	TGGCAAGCGTGCAAGGTTCAAGAGAGGAAGCTTCGAGTATACCTTTCATTTGCAACAACA	1380
Db	1321	TGGCAAGCGTGCAAGGTTCAAGAGAGGAAGCTTCGAGTATACCTTTCATTTGCAACAACA	1380
Qy	1381	CTGACAAATCCAAGGTATATAAGAGGAGATTTAACTCTGTATGCCATAAACTCCATAACG	1440
Db	1381	CTGACAAATCCAAGGTATATAAGAGGAGATTTAACTCTGTATGCCATAAACTCCATAACG	1440
Qy	1441	TCACCAAGTACTTGGGTTACCTTATCTTTTCTAAACAAGAGTGGATAAATACCTTC	1500
Db	1441	TCACCAAGTACTTGGGTTACCTTATCTTTTCTAAACAAGAGTGGATAAATACCTTC	1500
Qy	1501	TAAGACCTTTGGGACCTCATGGATTTCTTCCAAATCTGTCCCACTCAATGGTCTTAACTC	1560
Db	1501	TAAGACCTTTGGGACCTCATGGATTTCTTCCAAATCTGTCCCACTCAATGGTCTTAACTC	1560
Qy	1561	TAAAGATGGTGGATGATCAAAACCTTGGCACCTTTAATGGAAAAACCTCTCCGGCCAGGAA	1620
Db	1561	TAAAGATGGTGGATGATCAAAACCTTGGCACCTTTAATGGAAAAACCTCTCCGGCCAGGAA	1620
Qy	1621	GTTTCACTGGGCTTGCCAGCTTTCTCATATAGTTTTTTTGTGATAAGAAATGCCAAAGTTG	1680
Db	1621	GTTTCACTGGGCTTGCCAGCTTTCTCATATAGTTTTTTTGTGATAAGAAATGCCAAAGTTG	1680

Qy 1681 CTGCTTGCATCTGAAATAAATAATATACTAGTCTGACACTG 1721  
Db 1681 CTGCTTGCATCTGAAATAAATAATATACTAGTCTGACACTG 1721

## RESULT 10

AD48717  
ID ADM48717 standard; cDNA; 1721 BP.

XX AC AD48717;

XX 03-JUN-2004 (first entry)

XX Human hpa cDNA.

XX Transgenic animal; heparanase; cancer; viral infection; restenosis;  
KW neurodegenerative disease; atherosclerosis; pulmonary disorder; hpa;  
XX human; gene; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

XX CDS 63..1694

XX /\*tag= a

XX /product= "Hpa protein"

XX US2003217375-A1.

XX 20-NOV-2003.

XX 24-FEB-2003; 2003US-00371218.

XX 31-AUG-1998; 98MO-US017954.

XX 01-MAR-1999; 99US-00258892.

XX 06-FEB-2001; 2001US-00776874.

XX 19-NOV-2001; 2001US-00988113.

XX (ZCHA/) ZCHARIA E.

XX (VLOD/) VLODAVSKY I.

XX (METZ/) METZGER S.

XX (PECK/) PECKER I.

XX (ILAN/) ILAN N.

XX (CHAJ/) CHAJEK-SHAUL T.

XX (GOLD/) GOLDSHMIDT O.

PI Zcharia E, Vlodavsky I, Metzger S, Pecker I, Ilan N;

PI Chajek-Shaul T, Goldshmidt O;

XX WPI; 2004-021918/02.

XX P-PSDB; ADM48716.

XX New transgenic non-human animal expressing heparinase, useful as models  
PT for human disease, such as cancers, viral infection, neurodegenerative  
PT diseases, restenosis, atherosclerosis and pulmonary disorders.

XX Example 1; SEQ ID NO 11; 106pp; English.

XX The present invention relates to a transgenic non-human animal whose  
CC genome comprises an exogenous polynucleotide sequence, including a  
CC promoter active in tissues of the non-human, a region encoding a human  
CC heparanase, where the promoter and the region encoding human heparanase  
CC are operably linked in the exogenous polynucleotide such that human  
CC heparanase is expressed in at least a portion of the cells of the non-  
CC human animal. The methods and compositions of the present invention are  
CC useful for the production of transgenic animals expressing heparanase, to  
CC be used as models for human diseases such as cancers, viral infection,  
CC restenosis, neurodegenerative diseases, atherosclerosis and pulmonary  
CC disorders. The present sequence is human hpa cDNA used in the  
CC exemplification of the invention.

XX Sequence 1721 BP; 451 A; 413 C; 410 G; 447 T; 0 U; 0 Other;

Query Match 99.9%; Score 1719.4; DB 12; Length 1721;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1720; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 1 CTAGAGCTTTGAGCTCTCCGCTGCGGCGAGCTGCGGGGGAGACGACAGGTGAGGCCA 60  
Db 1 CTAGAGCTTTGAGCTCTCCGCTGCGGCGAGCTGCGGGGGAGACGACAGGTGAGGCCA 60  
Qy 61 AGATGCTGTGCTGCGCTCGAAGCCTGCGCGCGCGCTGATGCTGCTCTCTCTGGGC 120  
Db 61 AGATGCTGTGCTGCGCTCGAAGCCTGCGCGCGCGCTGATGCTGCTCTCTCTGGGC 120  
Qy 121 CGCTGGGTCCCTCTCCCTGCGGCGCTGCGCGCGCGCTGATGCTGCTCTCTCTGGGC 180  
Db 121 CGCTGGGTCCCTCTCCCTGCGGCGCTGCGCGCGCGCTGATGCTGCTCTCTCTGGGC 180  
Qy 181 ACCTGAGCTCTTTCACCCAGGAGCGCTGACCTGCTGAGCCCTCTGTTCTCTCTGCTCA 240  
Db 181 ACCTGAGCTCTTTCACCCAGGAGCGCTGACCTGCTGAGCCCTCTGTTCTCTCTGCTCA 240  
Qy 241 CCATTGACGCCAACCTGGGCCACGAGCCGCGGTTCTCTCATCTCTCTGGGTTCTCCAAAGC 300  
Db 241 CCATTGACGCCAACCTGGGCCACGAGCCGCGGTTCTCTCATCTCTCTGGGTTCTCCAAAGC 300  
Qy 301 TTCGTACCTTGGCCAGAGGCTTGTCTCTGCGTACCTGAGGTTTGGTGCCACCAAGACAG 360  
Db 301 TTCGTACCTTGGCCAGAGGCTTGTCTCTGCGTACCTGAGGTTTGGTGCCACCAAGACAG 360  
Qy 361 ACTTCTCTAATTTTCGATCCCAAGAGGATCAACCTTTGAAGAGAGAGTTACTGGCAAT 420  
Db 361 ACTTCTCTAATTTTCGATCCCAAGAGGATCAACCTTTGAAGAGAGAGTTACTGGCAAT 420  
Qy 421 CTCAGTCAACAGGATATTTGCAAAATATGGATCCATCCCTCTCTGATGTGGAGAGAGT 480  
Db 421 CTCAGTCAACAGGATATTTGCAAAATATGGATCCATCCCTCTCTGATGTGGAGAGAGT 480  
Qy 481 TACGGTTGGAATGGCCCTACAGAGCAATGCTACTCCAGAACACTACAGAAAAGT 540  
Db 481 TACGGTTGGAATGGCCCTACAGAGCAATGCTACTCCAGAACACTACAGAAAAGT 540  
Qy 541 TCAAGAACAGCACTACTCAAGAGCTCTGATGCTATACACTTTTGGCAACTGCT 600  
Db 541 TCAAGAACAGCACTACTCAAGAGCTCTGATGCTATACACTTTTGGCAACTGCT 600  
Qy 601 CAGGACTGGACTTTGATCTTTGGCTAAATGCGTTATTAAGAACAGCAGATTTGCAGTGA 660  
Db 601 CAGGACTGGACTTTGATCTTTGGCTAAATGCGTTATTAAGAACAGCAGATTTGCAGTGA 660  
Qy 661 ACAGTTCTAATGCTCAGTTGCTCTCGACTACTGCTCTTCCAAAGGGGTATAACATTTCTT 720  
Db 661 ACAGTTCTAATGCTCAGTTGCTCTCGACTACTGCTCTTCCAAAGGGGTATAACATTTCTT 720  
Qy 721 GGAACCTAGCAATGAACCTTAACAGTTTCTTAAGAGGCTGATATTTTCATCAATGGT 780  
Db 721 GGAACCTAGCAATGAACCTTAACAGTTTCTTAAGAGGCTGATATTTTCATCAATGGT 780  
Qy 781 CGCAGTTAGGAGAGATTTTATTTCAATTTGATATAAATTTCTTAAGAAAGTCCACCTTCAAAA 840  
Db 781 CGCAGTTAGGAGAGATTTTATTTCAATTTGATATAAATTTCTTAAGAAAGTCCACCTTCAAAA 840  
Qy 841 ATCAAAACTCTATGCTGCTGATGTTGGTCCAGCTCGAAGAAAGACGGCTAAGATGCTGA 900  
Db 841 ATCAAAACTCTATGCTGCTGATGTTGGTCCAGCTCGAAGAAAGACGGCTAAGATGCTGA 900  
Qy 901 AGAGCTTCTGAGGCTGGTGGAGAGTGAATTCATTGATTCAGTTACATGCATCCTACTATT 960  
Db 901 AGAGCTTCTGAGGCTGGTGGAGAGTGAATTCATTGATTCAGTTACATGCATCCTACTATT 960  
Qy 961 TGAATGAGCGACTGCTTACCGAGGAGATTTTCTAAACCTCTGATGATTTGGACATTTTAA 1020  
Db 961 TGAATGAGCGACTGCTTACCGAGGAGATTTTCTAAACCTCTGATGATTTGGACATTTTAA 1020  
Qy 1021 TTTTCATCTGTGCAAAAGTTTTCAGGTTGTTGAGAGCAACAGGCTGGCAAGAGGTCT 1080

Db 1021 TTTTCATCTGTCCAAAAGATTTTCCAGGTGGTTGAGAGCACACAGCGCTGGCAAGAGTCT 1080  
Qy 1081 GGTTAGGAGAAACAAGCTCTGCATATGAGGCGGAGCGCCCTTGCTATFCGACACCTTTTG 1140  
Db 1081 GGTTAGGAGAAACAAGCTCTGCATATGAGGCGGAGCGCCCTTGCTATFCGACACCTTTTG 1140  
Qy 1141 CAGCTGGCTTTATGTGGCTGATATAATTTGGGCTGTGAGCCGATGGATAGAAAGTGG 1200  
Db 1141 CAGCTGGCTTTATGTGGCTGATATAATTTGGGCTGTGAGCCGATGGATAGAAAGTGG 1200  
Qy 1201 TGATGAGCAAGTATTTCTTTGGAGCAGGAAACTACCAATTTAGTGGATGAAACCTTCGATC 1260  
Db 1201 TGATGAGCAAGTATTTCTTTGGAGCAGGAAACTACCAATTTAGTGGATGAAACCTTCGATC 1260  
Qy 1261 CTTTACCTGATTTATGGCTATCTCTCTGTTCAAGAAATTTGGTGGGCCACCAAGGTGTTAA 1320  
Db 1261 CTTTACCTGATTTATGGCTATCTCTCTGTTCAAGAAATTTGGTGGGCCACCAAGGTGTTAA 1320  
Qy 1321 TGSCAAGCGTCAAGGTTCAAGAGAGGAGGCTTCGAGTATACCTTTTCATTTGCAACAACA 1380  
Db 1321 TGGCAAGCGTCAAGGTTCAAGAGAGGAGGCTTCGAGTATACCTTTTCATTTGCAACAACA 1380  
Qy 1381 CTGACAATCCAAAGGTATAAAGAGGAGATTTAACTCTGTATGCCATAAACCTCCATAACG 1440  
Db 1381 CTGACAATCCAAAGGTATAAAGAGGAGATTTAACTCTGTATGCCATAAACCTCCATAACG 1440  
Qy 1441 TCACAAGTACTTCGGGTTACCTTATCTTTTCTTAAAGCAAGTGGATAAATACCTTC 1500  
Db 1441 TCACAAGTACTTCGGGTTACCTTATCTTTTCTTAAAGCAAGTGGATAAATACCTTC 1500  
Qy 1501 TAAGACCTTTGGGACCTCATGATTAATTTCCAAATCTGTCRAACTCAATGGTCTAACTC 1560  
Db 1501 TAAGACCTTTGGGACCTCATGATTAATTTCCAAATCTGTCRAACTCAATGGTCTAACTC 1560  
Qy 1561 TAAAGATGGTGGATGATCAAAACCTTTGCCACCTTTTAAATGGMAAAACCTCTCGGCGCAGAA 1620  
Db 1561 TAAAGATGGTGGATGATCAAAACCTTTGCCACCTTTTAAATGGMAAAACCTCTCGGCGCAGAA 1620  
Qy 1621 GTTCACCTGGGCTTCCAGCTTTCTCATATAGTTTTTTTGTGATAAGAAATGCCAAAGTTG 1680  
Db 1621 GTTCACCTGGGCTTCCAGCTTTCTCATATAGTTTTTTTGTGATAAGAAATGCCAAAGTTG 1680  
Qy 1681 CTGCTTGCATCTGAATAAATAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1721  
Db 1681 CTGCTTGCATCTGAATAAATAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1721

RESULT 11

AD48715  
ID ADM48715 standard; cDNA; 1721 BP.  
XX AC  
XX AC  
XX AC  
DT 03-JUN-2004 (first entry)  
XX AC  
DE Human hpa cDNA.  
XX  
KW Transgenic animal; heparanase; cancer; viral infection; restenosis;  
KW neurodegenerative disease; atherosclerosis; pulmonary disorder; hpa;  
KW human; gene; ss.  
XX  
OS Homo sapiens.  
XX  
XX  
FH Key Location/Qualifiers  
FT CDS 63..1694  
FT /\*tag= a  
FT /product= "Hpa protein"  
XX  
XX US2003217375-A1.  
XX 20-NOV-2003.  
XX

Query Match 99.9% Score 1719,4; DB 12; Length 1721;  
Best Local Similarity 99.9%; Pred.No. 0;  
Matches 1720; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 1 CTAGAGCTTTTCGACTCTCCGCTCGCGGCGAGCTGGCGGGGGAGCAGCCAGGTGAGCCCA 60  
Db 1 CTAGAGCTTTTCGACTCTCCGCTCGCGGCGAGCTGGCGGGGGAGCAGCCAGGTGAGCCCA 60  
Qy 61 AGATGCTGTGCGCTGGAAGCCTGCGCTGCGCGCGCGCTGATGCTGCTGCTGCTGCGGC 120  
Db 61 AGATGCTGTGCGCTGGAAGCCTGCGCTGCGCGCGCGCTGATGCTGCTGCTGCTGCGGC 120  
Qy 121 CGCTGGGTCCCTCTCCCTGCGCGCCTGCGCGCGCGCTGATGCTGCTGCTGCTGCGGC 180  
Db 121 CGCTGGGTCCCTCTCCCTGCGCGCCTGCGCGCGCGCTGATGCTGCTGCTGCTGCGGC 180  
Qy 181 ACCTGGACTTTTTCACCCAGGAGCGCTGACCTGTGAGCCCTCGTCTGCTGCTGCTGCTCA 240  
Db 181 ACCTGGACTTTTTCACCCAGGAGCGCTGACCTGTGAGCCCTCGTCTGCTGCTGCTGCTCA 240  
Qy 241 CCATTGACGCAACCTGGCCACGGAACCCGCGGTTCCTCATCTCTCTGCTGCTGCTGCTCA 300  
Db 241 CCATTGACGCAACCTGGCCACGGAACCCGCGGTTCCTCATCTCTCTGCTGCTGCTGCTCA 300  
Qy 301 TTGCTACCTTTGGCCAGAGGCTTGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360  
Db 301 TTGCTACCTTTGGCCAGAGGCTTGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360  
Qy 361 ACTTCTTAATTTTCGATCCCAAGAGGAATCAACCTTTTGAAGAGAGAGTACTTGGCAAT 420  
Db 361 ACTTCTTAATTTTCGATCCCAAGAGGAATCAACCTTTTGAAGAGAGAGTACTTGGCAAT 420

24-FEB-2003; 2003US-00371218.  
31-AUG-1998; 98WO-US017954.  
01-MAR-1999; 99US-00258892.  
06-FEB-2001; 2001US-00776874.  
19-NOV-2001; 2001US-00988113.  
(ZCHA/) ZCHARIA E.  
(VLJD/) VLJDAVSKY I.  
(METZ/) METZGER S.  
(PECK/) PECKER I.  
(ILAN/) ILAN N.  
(CHAJ/) CHAJEK-SHAUL T.  
(GOLD/) GOLDSHMIDT O.  
Zcharia E, Vlodavsky I, Metzger S, Pecker I, Ilan N;  
Chajek-Shaul T, Goldshmidt O;  
WPI: 2004-021918/02.  
P-PSDB; ADM48716.  
New transgenic non-human animal expressing heparinase, useful as models  
for human disease, such as cancers, viral infection, neurodegenerative  
diseases, restenosis, atherosclerosis and pulmonary disorders.  
Example 1; SEQ ID NO 9; 106pp; English.

The present invention relates to a transgenic non-human animal whose  
genome comprises an exogenous polynucleotide sequence, including a  
promoter active in tissues of the non-human, a region encoding a human  
heparanase, where the promoter and the region encoding human heparanase  
are operably linked in the exogenous polynucleotide such that human  
heparanase is expressed in at least a portion of the cells of the non-  
human animal. The methods and compositions of the present invention are,  
useful for the production of transgenic animals expressing heparanase, to  
be used as models for human diseases such as cancers, viral infection,  
restenosis, neurodegenerative diseases, atherosclerosis and pulmonary  
disorders. The present sequence is human hpa cDNA used in the  
exemplification of the invention.

Sequence 1721 BP; 451 A; 413 C; 410 G; 447 T; 0 U; 0 Other;

Qy	421	CTCAAGTCAACAGGATATTTGCAAAATATGGATCCATCCCTCCTGATGTGGAGGAGAAGT	480
Db	421	CTCAAGTCAACAGGATATTTGCAAAATATGGATCCATCCCTCCTGATGTGGAGGAGAAGT	480
Qy	481	TACGGTTGGAATGGCCCTACAGAGCAATTTGCTACTCCAGAACACTACAGAAAAGT	540
Db	481	TACGGTTGGAATGGCCCTACAGAGCAATTTGCTACTCCAGAACACTACAGAAAAGT	540
Qy	541	TCAAGAACAGCACTACTCAAGAGCTCTGTAGATGTCTATACACTTTTGGCAAACTGCT	600
Db	541	TCAAGAACAGCACTACTCAAGAGCTCTGTAGATGTCTATACACTTTTGGCAAACTGCT	600
Qy	601	CAGGACTGGACTTGATCTTTGGCCATAATGCTTTATTAAGAACAGCAGATTTGCAGTGA	660
Db	601	CAGGACTGGACTTGATCTTTGGCCATAATGCTTTATTAAGAACAGCAGATTTGCAGTGA	660
Qy	661	ACAGTCTTAATGCTCAGTGTGCTGCACTACTGCTCTTCCAAAGGGGTATAAATTTCTT	720
Db	661	ACAGTCTTAATGCTCAGTGTGCTGCACTACTGCTCTTCCAAAGGGGTATAAATTTCTT	720
Qy	721	GGGAACCTAGCAATGAACCTAAACAGTTTCTTAAAGAGGCTGATATTTTTCATCAATGGGT	780
Db	721	GGGAACCTAGCAATGAACCTAAACAGTTTCTTAAAGAGGCTGATATTTTTCATCAATGGGT	780
Qy	781	CGCAGTTAGGAGAGATTTTATTCAATTCATATAAATCTTAAAGAAAGTCCACCTTCAAAA	840
Db	781	CGCAGTTAGGAGAGATTTTATTCAATTCATATAAATCTTAAAGAAAGTCCACCTTCAAAA	840
Qy	841	ATGCAAACTCTATGTCCTGATGTTGGTCAAGCTTGAAGAAAGAGCGCTTAAGATGCTGA	900
Db	841	ATGCAAACTCTATGTCCTGATGTTGGTCAAGCTTGAAGAAAGAGCGCTTAAGATGCTGA	900
Qy	901	AGAGCTTCCTGAAGGCTGGAGAGTGAATTCAGTTACATGCGATCACTACTATT	960
Db	901	AGAGCTTCCTGAAGGCTGGAGAGTGAATTCAGTTACATGCGATCACTACTATT	960
Qy	961	TGAATGACCGGACTGCTACCAAGGAGATTTTCTAAACCTTGATGTATTGGACATTTTAA	1020
Db	961	TGAATGACCGGACTGCTACCAAGGAGATTTTCTAAACCTTGATGTATTGGACATTTTAA	1020
Qy	1021	TTTCACTCTGCAAAAAGTTTTCAGGTGTGAGAGCACAGGCTTGGCAAGAGTCT	1080
Db	1021	TTTCACTCTGCAAAAAGTTTTCAGGTGTGAGAGCACAGGCTTGGCAAGAGTCT	1080
Qy	1081	GGTTAGGAGAAACAAGCTCTGCATATGGAGCGGAGCGCCCTTGCTATCCGACACCTTTC	1140
Db	1081	GGTTAGGAGAAACAAGCTCTGCATATGGAGCGGAGCGCCCTTGCTATCCGACACCTTTC	1140
Qy	1141	CAGTGGCTTTATGTGGCTGGATAAATTTGGGCTGTTCAGCCCGAATGGGAATAGAAGTGG	1200
Db	1141	CAGTGGCTTTATGTGGCTGGATAAATTTGGGCTGTTCAGCCCGAATGGGAATAGAAGTGG	1200
Qy	1201	TGATGAGGCAAGTATTTCTTTGGAGCAGGAATACCAATTTAGTGGATGAATACTTCGATC	1260
Db	1201	TGATGAGGCAAGTATTTCTTTGGAGCAGGAATACCAATTTAGTGGATGAATACTTCGATC	1260
Qy	1261	CTTTACTGATTTATGCTATCTTCTTCTGTTCAAGAAATTTGGTGGGACCAAGGTGTAA	1320
Db	1261	CTTTACTGATTTATGCTATCTTCTTCTGTTCAAGAAATTTGGTGGGACCAAGGTGTAA	1320
Qy	1321	TGGCAAGCTGCAAGGTTTCAAGAGAGGAGCTTTCAGATATACCTTCATTGACAAACA	1380
Db	1321	TGGCAAGCTGCAAGGTTTCAAGAGAGGAGCTTTCAGATATACCTTCATTGACAAACA	1380
Qy	1381	CTGCAATCCAGGTATAAAGAGGAGATTTAACTCTGTATGCCATAAACTCCATAACG	1440
Db	1381	CTGCAATCCAGGTATAAAGAGGAGATTTAACTCTGTATGCCATAAACTCCATAACG	1440
Qy	1441	TCACCAAGTACTTGGGTTACCTATCTTTTCTAACAGCAAGTGGATAATACCTTC	1500
Db	1441	TCACCAAGTACTTGGGTTACCTATCTTTTCTAACAGCAAGTGGATAATACCTTC	1500

Qy	1501	TAAGACCTTTGGGACCTCATGGATTACTTTCCAAATCTGTCCAACCTCAATGGTCTAACTC	1560
Db	1501	TAAGACCTTTGGGACCTCATGGATTACTTTCCAAATCTGTCCAACCTCAATGGTCTAACTC	1560
Qy	1561	TAAAGATGTGGATGATCAAACTTCCACCTTTTAATGGAATAACCTCTCCGGCCAGGAA	1620
Db	1561	TAAAGATGTGGATGATCAAACTTCCACCTTTTAATGGAATAACCTCTCCGGCCAGGAA	1620
Qy	1621	GTTCACTGGGCTTCCAGGCTTTCTCATATAGTTTTTTTGTGATAAGAAATGCCAAAGTTG	1680
Db	1621	GTTCACTGGGCTTCCAGGCTTTCTCATATAGTTTTTTTGTGATAAGAAATGCCAAAGTTG	1680
Qy	1681	CTGCTTGCATCTGAAATAAATAATATATAGTCTGACACTG	1721
Db	1681	CTGCTTGCATCTGAAATAAATAATATATAGTCTGACACTG	1721

RESULT 12  
AEA42434  
ID AEA42434 standard; cDNA; 1721 BP.  
XX  
AC AEA42434;  
XX  
DT 28-JUL-2005 (first entry)  
XX  
Human heparanase encoding cDNA SEQ ID NO:12.  
XX  
DE antibody; heparanase; antiinflammatory; vulnery; immunosuppressive;  
XX  
KW antitumor; cytostatic; antiarteriosclerotic; vasotropic;  
KW inflammation; wound healing; scarring; vasculopathy; autoimmune disease;  
KW angiogenesis disorder; cancer; tumor; metastasis; gene; ss.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT CDS 63..1694  
FT FT /\*tag= a  
FT FT /product= "heparanase"  
FT FT /transl\_except= (pos:798..800,aa:Phe)  
FT FT /notes= "in SEQ ID NO:4, the corresponding protein in  
FT FT figure 47 decodes exactly"  
XX  
XX AU2004201462-A1.  
XX  
XX 06-MAY-2004.  
XX  
XX 08-APR-2004; 2004AU-00201462.  
XX  
XX 08-APR-2004; 2004AU-00201462.  
XX  
XX (INSI-) INSIGHT BIOPHARMACEUTICALS LTD.  
XX (HADA-) HADASIT MEDICAL RES SERVICES & DEV LTD.  
XX  
XX Vlodavsky I, Pecker I, Miron M, Gilboa A, Miron D, Moskowitz H;  
PI Shlomi Y, Peleg Y, Yacoby-Zeevi O, Ayal-Hershkovitz M, Ben-Artzi H;  
PI Feinstein E;  
XX  
XX WPI; 2005-173343/19.  
XX  
XX P-PSDB; AEA42426, AEA42466.  
XX  
XX Novel isolated antibody capable of specifically binding to epitope of  
PT heparanase protein, useful for preventing and treating heparanase-related  
PT disorder such as inflammatory disorder, scars, autoimmune conditions or  
PT angiogenesis.  
XX  
XX Example 7; SEQ ID NO 12; 260pp; English.  
XX  
XX The invention relates to an isolated antibody or its portion (I) capable  
CC of specifically binding to an epitope of a heparanase protein. Also  
CC described: (1) a cell line (II) for producing a monoclonal antibody or  
CC its portion, comprising a cell line for producing (I); (2) a  
CC pharmaceutical composition comprising (I) and a carrier; and (3) an  
CC affinity medium (III) for binding human heparanase polypeptides,



CC comprising (I) immobilized to a chemically inert, insoluble carrier. (I)  
 CC useful for treating a subject suffering from a pathological condition,  
 CC which involves administering (I) to the subject. (I) is useful for  
 CC preventing and treating heparanase-related disorder or condition chosen  
 CC from inflammatory disorder, wound, scar, vasculopathy, autoimmune  
 CC condition, angiogenesis, cell proliferation, cancerous condition, tumor  
 CC cell proliferation, invasion of circulating tumor cells and metastatic  
 CC disease. (I) is useful for detecting the presence of heparanase  
 CC polypeptide in a sample. (I) is useful for detecting heparanase-related  
 CC disease or condition in a subject such as vertebrate, preferably mammal  
 CC e.g., human. The heparanase-related disorder or condition further  
 CC includes renal disease or disorder chosen from diabetic nephropathy,  
 CC glomerulosclerosis, nephrotic syndrome, minimal change nephrotic syndrome  
 CC and renal cell carcinoma. The present sequence encodes human heparanase,  
 CC which is used in the exemplification of the present invention.

XX  
 SQ Sequence 1721 BP; 451 A; 413 C; 410 G; 447 T; 0 U; 0 Other;

Query Match 99.9%; Score 1719.4; DB 14; Length 1721;  
 Best Local Similarity 99.9%; Pred. No. 0;  
 Matches 1720; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CTAGAGCTTTGACTCTCCGTCGCGCAGCTGGCGGGGGAGCAGCCAGGTGAGCCCA 60  
 Db 1 CTAGAGCTTTGACTCTCCGTCGCGCAGCTGGCGGGGGAGCAGCCAGGTGAGCCCA 60

Qy 61 AGATGCTGCTGCGCTCGAAGCTGCGTGGCGCGCGCGCTGATGCTGCTGCTGGGC 120  
 Db 61 AGATGCTGCTGCGCTCGAAGCTGCGTGGCGCGCGCGCTGATGCTGCTGCTGGGC 120

Qy 121 CGCTGGGTGCCCTCTCCCTGGCGCCTGCCCGCAGCTGGCAGCAGAGCTGCTGG 180  
 Db 121 CGCTGGGTGCCCTCTCCCTGGCGCCTGCCCGCAGCTGGCAGCAGAGCTGCTGG 180

Qy 181 ACCTGGACTTTCTTCCACCAGAGCGCTGCACTGGTGAGCCCTCGTTCTGTCGCTCA 240  
 Db 181 ACCTGGACTTTCTTCAACCAGAGCGCTGCACTGGTGAGCCCTCGTTCTGTCGCTCA 240

Qy 241 CCATTGAGCGCAACTGGCCAGCAGCGGGTTCCTCATCTCTCTGGGTTCCTCAAGC 300  
 Db 241 CCATTGAGCGCAACTGGCCAGCAGCGGGTTCCTCATCTCTCTGGGTTCCTCAAGC 300

Qy 301 TTCTGTACTTGGCCAGAGGCTTGCTCTCTGGTACCTGAGGTTGGTGCCACCAAGACAG 360  
 Db 301 TTCTGTACTTGGCCAGAGGCTTGCTCTCTGGTACCTGAGGTTGGTGCCACCAAGACAG 360

Qy 361 ACTTCCTAAATTTTCGATCCCAAGAAGGAATCAACCTTTGAAGAGAGAAGTTACTGGCAAT 420  
 Db 361 ACTTCCTAAATTTTCGATCCCAAGAAGGAATCAACCTTTGAAGAGAGAAGTTACTGGCAAT 420

Qy 421 CTCAAGTCAACCAGGATATTTGCAAAATATGGATCCATCCCTCTCTGATGTGGAGAGAAT 480  
 Db 421 CTCAAGTCAACCAGGATATTTGCAAAATATGGATCCATCCCTCTCTGATGTGGAGAGAAT 480

Qy 481 TACGGTTGGATGCGCCTACCAGAGCAATTTGCTACTCCGAGAACACTACCAGAAAAGT 540  
 Db 481 TACGGTTGGATGCGCCTACCAGAGCAATTTGCTACTCCGAGAACACTACCAGAAAAGT 540

Qy 541 TCAAGAAGCAGCACCTACTCAAGAAGCTCTGTAGATGTGCTATACACTTTTGCAAACTGCT 600  
 Db 541 TCAAGAAGCAGCACCTACTCAAGAAGCTCTGTAGATGTGCTATACACTTTTGCAAACTGCT 600

Qy 601 CAGGACTGGACTTGATCTTTGGCCCTAAATGGGTTATTAAGAACAGAGATTTGAGTGA 660  
 Db 601 CAGGACTGGACTTGATCTTTGGCCCTAAATGGGTTATTAAGAACAGAGATTTGAGTGA 660

Qy 661 ACAGTCTTAATGCTCAGTGTCTCTGGACTACTGCTCTTCCAGGGGTATAACATTTCTT 720  
 Db 661 ACAGTCTTAATGCTCAGTGTCTCTGGACTACTGCTCTTCCAGGGGTATAACATTTCTT 720

Qy 721 GGGAACTAGGCAATGAACCTAACAGTTTCTTAAAGAGGCTGTATATTTTCATCAATGGGT 780  
 Db 721 GGGAACTAGGCAATGAACCTAACAGTTTCTTAAAGAGGCTGTATATTTTCATCAATGGGT 780

RESULT 13  
 AEA42435  
 ID AEA42435 standard; cdna; 1721 BP.  
 XX  
 AC AEA42435;  
 XX  
 DT 28-JUL-2005 (first entry)

Qy 781 CGCAGTTAGGAGAGATTTTATTCAATTCATATAAATCTTCTAAGAAAGTCCACCTTCAAAA 840  
 Db 781 CGCAGTTAGGAGAGATTTTATTCAATTCATATAAATCTTCTAAGAAAGTCCACCTTCAAAA 840

Qy 841 ATGCAAAACTCTATGGTCTCTGATGTTGGTCTGAGCTCGAAGAAAGACGGCTTAAGATGCTGA 900  
 Db 841 ATGCAAAACTCTATGGTCTCTGATGTTGGTCTGAGCTCGAAGAAAGACGGCTTAAGATGCTGA 900

Qy 901 AGAGCTTCTGAAGGCTGTGGAGAGATGATTGATTGATTGATTGATTGATTGATTGATTGATT 960  
 Db 901 AGAGCTTCTGAAGGCTGTGGAGAGATGATTGATTGATTGATTGATTGATTGATTGATTGATT 960

Qy 961 TGAATGAGCAGGACTGCTTACCAGGAGAGATTTTCTTAAACCTGATGTATTCGACATTTTTTA 1020  
 Db 961 TGAATGAGCAGGACTGCTTACCAGGAGAGATTTTCTTAAACCTGATGTATTCGACATTTTTTA 1020

Qy 1021 TTTTCATCTGTGCAAAAAGTTTTTCCAGGTGGTGGAGACACCGAGCTTGGCAAGAAGTCT 1080  
 Db 1021 TTTTCATCTGTGCAAAAAGTTTTTCCAGGTGGTGGAGACACCGAGCTTGGCAAGAAGTCT 1080

Qy 1081 GGTTAGGAGAAAACAAGCTCTGATATGGAGCGGAGCGCCCTTGTCTATCCGACACCTTTG 1140  
 Db 1081 GGTTAGGAGAAAACAAGCTCTGATATGGAGCGGAGCGCCCTTGTCTATCCGACACCTTTG 1140

Qy 1141 CAGCTGCTTTTATGTGGCTGGATAAAATTTGGGCGCTGTGAGCCCGAATGGGAATAGAAGTGG 1200  
 Db 1141 CAGCTGCTTTTATGTGGCTGGATAAAATTTGGGCGCTGTGAGCCCGAATGGGAATAGAAGTGG 1200

Qy 1201 TGATGAGGCAAGTATTTTGGAGCAGGAACTACCATTTAGTGGATGAAACCTTCGATC 1260  
 Db 1201 TGATGAGGCAAGTATTTTGGAGCAGGAACTACCATTTAGTGGATGAAACCTTCGATC 1260

Qy 1261 CTTTACCTGATATGCGCTATCTCTCTGTTTCAAGAAAATTTGGTGGGCAACCAAGGTGTAA 1320  
 Db 1261 CTTTACCTGATATGCGCTATCTCTCTGTTTCAAGAAAATTTGGTGGGCAACCAAGGTGTAA 1320

Qy 1321 TGGCAAGCGTGAAGGTTCAAAGAGAGGAGCTTCGAGTATACCTTTCATTGACACAACA 1380  
 Db 1321 TGGCAAGCGTGAAGGTTCAAAGAGAGGAGCTTCGAGTATACCTTTCATTGACACAACA 1380

Qy 1381 CTGACAACTCAAGGTATTAAGAAAGAGAGATTTAACTCTGTATGCCATAAACCTCCATAACG 1440  
 Db 1381 CTGACAACTCAAGGTATTAAGAAAGAGAGATTTAACTCTGTATGCCATAAACCTCCATAACG 1440

Qy 1441 TCACCAAGTACTTGGGTTACCTATTCCTTTTCTAAAGAGAGGATTAATATACCTTC 1500  
 Db 1441 TCACCAAGTACTTGGGTTACCTATTCCTTTTCTAAAGAGAGGATTAATATACCTTC 1500

Qy 1501 TAAGACCTTTGGGACCTCATGGATTAATTTCCAAATCTGTCCAACTCAATGCTTAACCTC 1560  
 Db 1501 TAAGACCTTTGGGACCTCATGGATTAATTTCCAAATCTGTCCAACTCAATGCTTAACCTC 1560

Qy 1561 TAAAGATGGTGGATGATCAAAACCTTGGCACCTTTAATGGAAAAACCTCTCCGGCCAGGAA 1620  
 Db 1561 TAAAGATGGTGGATGATCAAAACCTTGGCACCTTTAATGGAAAAACCTCTCCGGCCAGGAA 1620

Qy 1621 GTTCACCTGGGCTGCCAGCTTCTCATATAGTTTTTTTGTGTGATAAGAAATGCCAAAGTTG 1680  
 Db 1621 GTTCACCTGGGCTGCCAGCTTCTCATATAGTTTTTTTGTGTGATAAGAAATGCCAAAGTTG 1680

Qy 1681 CTGCTTGCATCTGAAATAAAATATATCTAGTCTCTGCACCTG 1721  
 Db 1681 CTGCTTGCATCTGAAATAAAATATATCTAGTCTCTGCACCTG 1721



XX DE Human heparanase encoding cDNA SEQ ID NO:13.  
XX DE antibody; heparanase; antiinflammatory; vulnery; immunosuppressive;  
XX KW antiangiogenic; cytostatic; antiarteriosclerotic; vasotropic;  
XX KW inflammation; wound healing; scarring; vasculopathy; autoimmune disease;  
XX KW angiogenesis disorder; cancer; tumor; metastasis; gene; ss.  
XX OS Homo sapiens.  
XX FH Key Location/Qualifiers  
XX FT CDS 63..1694  
XX FT /\*tag= a  
XX FT /product= "heparanase"  
XX FT /transl\_except= (pos:798..800,aa:Phe)  
XX FT /note= "in SEQ ID NO:4, the corresponding protein in  
XX FT figure 47 decodes exactly"  
XX PN AU2004201462-A1.  
XX XX  
XX PD 06-MAY-2004.  
XX XX  
XX PF 08-APR-2004; 2004AU-00201462.  
XX XX  
XX PR 08-APR-2004; 2004AU-00201462.  
XX XX  
XX PA (INSI-) INSIGHT BIOPHARMACEUTICALS LTD.  
XX PA (HADA-) HADASIT MEDICAL RES SERVICES & DEV LTD.  
XX XX  
XX PI Vlodavsky I, Pecker I, Mimon M, Gilboa A, Miron D, Moskowitz H;  
XX PI Shlomi Y, Peleg Y, Yacoby-Zeevi O, Ayal-Hershkovitz M, Ben-Artzi H;  
XX PI Feinstein E;  
XX XX  
XX DR WPI; 2005-173343/19.  
XX DR P-PSDB; AEA42426, AEA42466.  
XX XX  
XX PT Novel isolated antibody capable of specifically binding to epitope of  
XX PT heparanase protein, useful for preventing and treating heparanase-related  
XX PT disorder such as inflammatory disorder, scars, autoimmune conditions or  
XX PT angiogenesis.  
XX XX  
XX PS Example 8; SEQ ID NO 13; 260pp; English.  
XX CC The invention relates to an isolated antibody or its portion (I) capable  
XX CC of specifically binding to an epitope of a heparanase protein. Also  
XX CC described: (1) a cell line (II) for producing a monoclonal antibody or  
XX CC its portion, comprising a cell line for producing (I); (2) a  
XX CC pharmaceutical composition comprising (I) and a carrier; and (3) an  
XX CC affinity medium (III) for binding human heparanase polypeptides,  
XX CC comprising (I) immobilized to a chemically inert, insoluble carrier. (I)  
XX CC useful for treating a subject suffering from a pathological condition,  
XX CC which involves administering (I) to the subject. (I) is useful for  
XX CC preventing and treating heparanase-related disorder or condition chosen  
XX CC from inflammatory disorder, wound, scar, vasculopathy, autoimmune  
XX CC condition, angiogenesis, cell proliferation, cancerous condition, tumor  
XX CC cell proliferation, invasion of circulating tumor cells and metastatic  
XX CC disease. (I) is useful for detecting the presence of heparanase  
XX CC polypeptide in a sample. (I) is useful for detecting heparanase-related  
XX CC disease or condition in a subject such as vertebrate, preferably mammal  
XX CC e.g., human. The heparanase-related disorder or condition further  
XX CC includes renal disease or disorder chosen from diabetic nephropathy,  
XX CC glomerulosclerosis, nephrotic syndrome, minimal change nephrotic syndrome  
XX CC and renal cell carcinoma. The present sequence encodes human heparanase,  
XX CC which is used in the exemplification of the present invention.  
XX XX  
XX SQ Sequence 1721 BP; 451 A; 413 C; 410 G; 447 T; 0 U; 0 Other;  
Query Match 99.9%; Score 1719.4; DB 14; Length 1721;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1720; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
1 CTAGAGCTTTCGACTCTCCGCTCGCGGCGAGCTGGGGGGGAGCAGCCAGGTGAGGCCA 60  
61 AGATGCTGCTGCGCTCGAAGCCTGCGCTGCGCGCGCGCTGATGCTGCTCTCTCTGGGC 120  
61 AGATGCTGCTGCGCTCGAAGCCTGCGCTGCGCGCGCGCTGATGCTGCTCTCTGGGC 120  
121 CGCTGGGTCCCTCTCCCTGCGGCGCTGCGCGCGCTGCGCGCGCTGCGCGCGCTGCG 180  
121 CGCTGGGTCCCTCTCCCTGCGGCGCTGCGCGCGCTGCGCGCGCTGCGCGCGCTGCG 180  
181 ACCTGGACTTCTTTCACCCAGGAGCGCTGCGCGCGCTGCGCGCGCTGCGCGCGCTGCG 240  
181 ACCTGGACTTCTTTCACCCAGGAGCGCTGCGCGCGCTGCGCGCGCTGCGCGCGCTGCG 240  
241 CCATTGACGCCAACCTGGCCACGAGCCGCGGTTCCTCATCTCTCTCTCTCTCTCTCT 300  
241 CCATTGACGCCAACCTGGCCACGAGCCGCGGTTCCTCATCTCTCTCTCTCTCTCTCT 300  
301 TTCGTACCTTGGCCAGAGGCTTGTCTCTCGGTACCTGAGGTTTGGTGGCACCAAGACAG 360  
301 TTCGTACCTTGGCCAGAGGCTTGTCTCTCGGTACCTGAGGTTTGGTGGCACCAAGACAG 360  
361 ACTTCTCTAATTTTCGATCCCAAGAGGAATCAACCTTTTGAAGAGAGAGTTTACTGGCAAT 420  
361 ACTTCTCTAATTTTCGATCCCAAGAGGAATCAACCTTTTGAAGAGAGAGTTTACTGGCAAT 420  
421 CTCAGTCAACACAGGATATTTGCAAAATATGGATCCATCCCTCTCTGATGTGGAGGAGT 480  
421 CTCAGTCAACACAGGATATTTGCAAAATATGGATCCATCCCTCTCTGATGTGGAGGAGT 480  
481 TAGCGTTGGAATGGCCCTTACCCAGGAGCAATGCTACTCCGAGAACACTACAGAAAAGT 540  
481 TAGCGTTGGAATGGCCCTTACCCAGGAGCAATGCTACTCCGAGAACACTACAGAAAAGT 540  
541 TCAAGAACAGCACTACTCAAGAGCTCTGTAGATGTGTATACATTTTTCGAAACTGCT 600  
541 TCAAGAACAGCACTACTCAAGAGCTCTGTAGATGTGTATACATTTTTCGAAACTGCT 600  
601 CAGGACTGGACTTGTATCTTTGGCTAAATGCGTTATTAAGAACAGCAGATTTGCGAGTGA 660  
601 CAGGACTGGACTTGTATCTTTGGCTAAATGCGTTATTAAGAACAGCAGATTTGCGAGTGA 660  
661 ACAGTTCTAATGCTCAGTTGCTCTCTGAGCTACTGCTCTTCCAAAGGGGTATAAATTTCTT 720  
661 ACAGTTCTAATGCTCAGTTGCTCTCTGAGCTACTGCTCTTCCAAAGGGGTATAAATTTCTT 720  
721 GCGAATGCGCATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATG 780  
721 GCGAATGCGCATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATG 780  
781 CGCAGTTAGGAGAGAGATTTTATTTCAATTTGATATAAATTTTCAAGAAAGTCCACCTTCAAAA 840  
781 CGCAGTTAGGAGAGAGATTTTATTTCAATTTGATATAAATTTTCAAGAAAGTCCACCTTCAAAA 840  
841 ATGCAAAACTCTATGCTCTGATGTTGGTCTGAGCTCTGAGAAAGAGCGGTAAAGTCTGA 900  
841 ATGCAAAACTCTATGCTCTGATGTTGGTCTGAGCTCTGAGAAAGAGCGGTAAAGTCTGA 900  
901 AGAGCTTCTGAGGCTGGTGGAGAGTGTATTCAGTTACATGTCATCCTACTACTT 960  
901 AGAGCTTCTGAGGCTGGTGGAGAGTGTATTCAGTTACATGTCATCCTACTACTT 960  
961 TGAATGAGCGGACTGCTACCCAGGAGAGATTTTCTAAACCTCTGATGTATTTGACATTTT 1020  
961 TGAATGAGCGGACTGCTACCCAGGAGAGATTTTCTAAACCTCTGATGTATTTGACATTTT 1020  
1021 TTTTCATCTGTGCAAAAAGTTCCTGAGTGGTTCGAGGCGGCGGCGGCTTCTATCGACACCTTTG 1080  
1021 TTTTCATCTGTGCAAAAAGTTCCTGAGTGGTTCGAGGCGGCGGCGGCTTCTATCGACACCTTTG 1080  
1081 GGTTAGGAGAAACAAGCTCTGCAATATGGAGGCGGCGGCGGCTTCTATCGACACCTTTG 1140  
1081 GGTTAGGAGAAACAAGCTCTGCAATATGGAGGCGGCGGCGGCTTCTATCGACACCTTTG 1140

Qy 1141 CAGCTGGCTTTATGTGGCTGTGATATAATGGGCCCTGTGAGCCCGAATGGGAATAGAAGTGG 1200  
Db 1141 CAGCTGGCTTTATGTGGCTGTGATATAATGGGCCCTGTGAGCCCGAATGGGAATAGAAGTGG 1200  
Qy 1201 TGATGAGCAAGTATTCTTTGGAGCAGGAAACTACCAATTTAGTGGATGAAGTTCGATC 1260  
Db 1201 TGATGAGCAAGTATTCTTTGGAGCAGGAAACTACCAATTTAGTGGATGAAGTTCGATC 1260  
Qy 1261 CTTTACCTGATATTGGCTATCTCTCTGTTCAAGAAATTTGGTGGGCACCAAGGTGTAA 1320  
Db 1261 CTTTACCTGATATTGGCTATCTCTCTGTTCAAGAAATTTGGTGGGCACCAAGGTGTAA 1320  
Qy 1321 TGGCAAGCGTCAAGGTTCAAGAGAGAGGAGCTTCGAGTATACCTTCATTTGACAAACA 1380  
Db 1321 TGGCAAGCGTCAAGGTTCAAGAGAGAGGAGCTTCGAGTATACCTTCATTTGACAAACA 1380  
Qy 1381 CTGACAATCCAAAGGTATAAGAGAGGAGATTTAACTCTGTATGCCATAAACCTCCATAACG 1440  
Db 1381 CTGACAATCCAAAGGTATAAGAGAGGAGATTTAACTCTGTATGCCATAAACCTCCATAACG 1440  
Qy 1441 TCACCAAGTACTTGGGTTACCTTATCTTTTCTTAACAAGCAAGTGGATAAATACCTTC 1500  
Db 1441 TCACCAAGTACTTGGGTTACCTTATCTTTTCTTAACAAGCAAGTGGATAAATACCTTC 1500  
Qy 1501 TAAGACCTTTGGGACCTCATGGATTACTTTCCAAATCTGTCCAACTCAATGGTCTAACTC 1560  
Db 1501 TAAGACCTTTGGGACCTCATGGATTACTTTCCAAATCTGTCCAACTCAATGGTCTAACTC 1560  
Qy 1561 TAAAGATGGTGGATGATCAAACTTGGCACCTTTAAATGGAAAAACCTCTCGGCCAGGAA 1620  
Db 1561 TAAAGATGGTGGATGATCAAACTTGGCACCTTTAAATGGAAAAACCTCTCGGCCAGGAA 1620  
Qy 1621 GTTCACTGGGCTTGGCAGCTTCTCATATAGTTTTTTTGTGATAGAAATGCCAAAGTTG 1680  
Db 1621 GTTCACTGGGCTTGGCAGCTTCTCATATAGTTTTTTTGTGATAGAAATGCCAAAGTTG 1680  
Qy 1681 CTGCTTGCATCTGAATAAATAATATACTAGTCCCTGACACTG 1721  
Db 1681 CTGCTTGCATCTGAATAAATAAATAATATACTAGTCCCTGACACTG 1721

RESULT 14

AA335650  
ID AA335650 standard; cdna; 1899 BP.

AC AA335650;  
XX

XX 09-JUL-1999 (first entry)  
DT

DE cDNA encoding a human heparanase protein.

XX Heparanase; hpa; modulator; heparin-binding growth factor;  
KW cellular response; cytokine; cell interaction; plasma lipoprotein;  
KW cellular susceptibility; infection; disintegration;  
KW neurodegenerative plaque; wound healing; angiogenesis; restenosis;  
KW atherosclerosis; inflammation; neurodegenerative disease; neutralise;  
KW plasma heparin; micrometastasis; autoimmune lesion; renal failure; ss.

XX Homo sapiens.  
OS

XX WO9911798-A1.  
PN

XX 11-MAR-1999.  
PD

XX 31-AUG-1998; 98WO-US017954.  
XX

XX 02-SEP-1997; 97US-00922170.  
XX

XX 02-JUL-1998; 98US-00109386.  
XX

XX (INSI-) INSIGHT STRATEGY & MARKETING LTD.  
XX (HADA-) HADASIT MEDICAL RES SERVICES & DEV.  
XX (FRIE/) FRIEDMAN M M.

XX Pecker I, Vlodavsky I, Feinstein E;  
XX WPI; 1999-302255/25.  
XX P-PSDB; AAY02346.  
XX New human polynucleotide useful for treating angiogenesis, restenosis,  
XX PT and inflammation.  
XX Claim 4; Page 64-65; 63pp; English.  
XX The specification describes a polypeptide having heparanase (hpa)  
XX activity. The recombinant protein is used as a modulator of heparin-  
XX binding growth factors, cellular responses to heparin-binding growth  
XX factors and cytokines, cell interaction with plasma lipoproteins,  
XX cellular susceptibility to viral, protozoal and bacterial infections or  
XX disintegration of neurodegenerative plaques. Heparanase may be useful for  
XX conditions such as wound healing, angiogenesis, restenosis,  
XX atherosclerosis, inflammation, neurodegenerative diseases, and viral  
XX infections. Mammalian heparanase can be used to neutralize plasma  
XX heparin, and anti-heparanase antibodies may be applied for  
XX immunodetection and diagnosis of micrometastases, autoimmune lesions, and  
XX renal failure in biopsy specimens, plasma samples, and body fluids. The  
XX present sequence encodes human heparanase

SQ Sequence 1899 BP; 495 A; 433 C; 510 G; 461 T; 0 U; 0 Other;

Query Match 99.8%; Score 1717.8; DB 2; Length 1899;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1719; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CTAGAGCTTTGCACTCTCCGCTCGCGGGAGCTGGGGGGGAGCAGCCAGGTGAGCCCA 60  
Db 179 CTAGAGCTCTGACTCTCCGCTCGCGGGAGCTGGGGGGGAGCAGCCAGGTGAGCCCA 238  
Qy 61 AGATGCTGCTGCGCTCGAAGCCTGCGCTGCGCGCGCGCTGATGCTGCTCTCTGGGGC 120  
Db 239 AGATGCTGCTGCGCTCGAAGCCTGCGCTGCGCGCGCGCTGATGCTGCTCTGGGGC 298  
Qy 121 CGCTGGGTCCCTCTCTCCCTGGCGCCCTGCCCGCAGCTGCGCAAGCAGCAGAGCTCTGG 180  
Db 299 CGCTGGGTCCCTCTCTCCCTGGCGCCCTGCCCGCAGCTGCGCAAGCAGCAGAGCTCTGG 358  
Qy 181 ACCTGGAATCTTTCACCCAGGAGCGCTGCACCTGGTGAGCCCTCTCTCTCTGCTCTCA 240  
Db 359 ACCTGGAATCTTTCACCCAGGAGCGCTGCACCTGGTGAGCCCTCTCTCTCTGCTCTCA 418  
Qy 241 CCATTGACGCGCAACCTGGCCACGAGCCCGCGGTTCTCTCATCTCTCTGGGTTCTCCAAAGC 300  
Db 419 CCATTGACGCGCAACCTGGCCACGAGCCCGCGGTTCTCTCATCTCTCTGGGTTCTCCAAAGC 478  
Qy 301 TTCGTACCTTGGCCAGAGGCTTGTCTCTCGGTACTCTGAGGTTTGGTGGCAGCAGACAG 360  
Db 479 TTCGTACCTTGGCCAGAGGCTTGTCTCTCGGTACTCTGAGGTTTGGTGGCAGCAGACAG 538  
Qy 361 ACTTCTTAATTTTCGATCCCAAGAGGAATCAACCTTTGAAGAGAGAGTACTTGGCAAT 420  
Db 539 ACTTCTTAATTTTCGATCCCAAGAGGAATCAACCTTTGAAGAGAGAGTACTTGGCAAT 598  
Qy 421 CTCAAGTCAACCCAGGATATTTGCAAAATATGGATCCATCCCTCTCTGTGTGGAGGAGAAGT 480  
Db 599 CTCAAGTCAACCCAGGATATTTGCAAAATATGGATCCATCCCTCTCTGTGTGGAGGAGAAGT 658  
Qy 481 TAGCGTTGGAATGGCCCTTACAGAGCAATTTGCTACTCCGAGAACACATACCAGAAAAAGT 540  
Db 659 TAGCGTTGGAATGGCCCTTACAGAGCAATTTGCTACTCCGAGAACACATACCAGAAAAAGT 718  
Qy 541 TCAAGAACAGCAGCTACTCTCAAGAGCTCTGATAGTGTCTATACACTTTTTCGAACTGCT 600  
Db 719 TCAAGAACAGCAGCTACTCTCAAGAGCTCTGATAGTGTCTATACACTTTTTCGAACTGCT 778  
Qy 601 CAGGACTGGACTTGTATCTTTGGCCCTAAATCGTTTATTAAAGAACAGAGATTGTCAGTGG 660

Db 779 CAGACTGGACTTGATCTTTGGCCCTAAATGCGTTATTAAAGAACAGCAGATTTCAGTGA 838  
Qy 661 ACAGTCTTAATGCTCAGTTGCTCTCGGACTACTGCTCTTCCAAAGGGGTATAACAATTTCTT 720  
Db 839 ACAGTCTTAATGCTCAGTTGCTCTCGGACTACTGCTCTTCCAAAGGGGTATAACAATTTCTT 898  
Qy 721 GGGAACTAGGCAATGAACCTAACAGTTTCCTTAAGAGGGGTGATATTTTCATCAATGGGT 780  
Db 899 GGGAACTAGGCAATGAACCTAACAGTTTCCTTAAGAGGGGTGATATTTTCATCAATGGGT 958  
Qy 781 CGCAGTTAGGAGAGAGATTTTATCAATGTCATAAATCTTAAAGAAAGTCACCTTCAAAA 840  
Db 959 CGCAGTTAGGAGAGAGATTTTATCAATGTCATAAATCTTAAAGAAAGTCACCTTCAAAA 1018  
Qy 841 ATGCAAACTCTATGGTCTGATGTTGGTTCAGCCCTCGAAGAAAGACCGCTAAGATGCTGA 900  
Db 1019 ATGCAAACTCTATGGTCTGATGTTGGTTCAGCCCTCGAAGAAAGACCGCTAAGATGCTGA 1078  
Qy 901 AGAGCTTCCTGAAGGCTGGTGGAGAAAGTATGATTCAGTTACATGCGATCACTACTATT 960  
Db 1079 AGAGCTTCCTGAAGGCTGGTGGAGAAAGTATGATTCAGTTACATGCGATCACTACTATT 1138  
Qy 961 TGATGACCGGACTGCTACCAAGGAAGATTTTCTAACCCTGATGATTTGGACATTTTAA 1020  
Db 1139 TGAATGACCGGACTGCTACCAAGGAAGATTTTCTAACCCTGATGATTTGGACATTTTAA 1198  
Qy 1021 TTTTCATCTGCAAAAAGTTTTCAGGTGGTGTAGAGCACCAGGCTGGCAAGAGGTCT 1080  
Db 1199 TTTTCATCTGCAAAAAGTTTTCAGGTGGTGTAGAGCACCAGGCTGGCAAGAGGTCT 1258  
Qy 1081 GGTTCAGGAAACAAAGCTCTGCATATGAGAGCGGAGCGCCCTTGCTATCCGACACCTTTG 1140  
Db 1259 GGTTCAGGAAACAAAGCTCTGCATATGAGAGCGGAGCGCCCTTGCTATCCGACACCTTTG 1318  
Qy 1141 CAGCTGCTTTATGCTGCTGATTAATTTGGCCCTGTGAGCCGAGTGGGAATAGAGTGG 1200  
Db 1319 CAGCTGCTTTATGCTGCTGATTAATTTGGCCCTGTGAGCCGAGTGGGAATAGAGTGG 1378  
Qy 1201 TGATGAGCGAAGTATTTCTTGGAGCAGAACTACCATTTAGTGGATGAAACCTTCGATC 1260  
Db 1379 TGATGAGCGAAGTATTTCTTGGAGCAGAACTACCATTTAGTGGATGAAACCTTCGATC 1438  
Qy 1261 CTTTACCTGATATTGCTATCTCTTCTGTTCAAGAAATTTGGTGGGCAACCAAGGTGTTAA 1320  
Db 1439 CTTTACCTGATATTGCTATCTCTTCTGTTCAAGAAATTTGGTGGGCAACCAAGGTGTTAA 1498  
Qy 1321 TGGCAAGCGTCAGGTTCAAGAGAGGAGCTTCGAGTATACCTTCATTCGACAAACA 1380  
Db 1499 TGGCAAGCGTCAGGTTCAAGAGAGGAGCTTCGAGTATACCTTCATTCGACAAACA 1558  
Qy 1381 CTGCAATCCAAGGTATAAGAGAGGAGATTAACTCTGTATGCCATAAACCTCCATAACG 1440  
Db 1559 CTGCAATCCAAGGTATAAGAGAGGAGATTAACTCTGTATGCCATAAACCTCCATAACG 1618  
Qy 1441 TCACCAAGTACTTCGGGTACCCCTATCTCTTTTCAACAGCAAGTGGATAAATACCTTC 1500  
Db 1619 TCACCAAGTACTTCGGGTACCCCTATCTCTTTTCAACAGCAAGTGGATAAATACCTTC 1678  
Qy 1501 TAAGACCTTTGGGACCTCATGATATCTTCCAAATCTGTCCAACTCAATGGTCTAACTC 1560  
Db 1679 TAAGACCTTTGGGACCTCATGATATCTTCCAAATCTGTCCAACTCAATGGTCTAACTC 1738  
Qy 1561 TAAAGATGGTGATGATCAACCTTGGCCACTTTAATGGAACCACTCTCCGGCCAGAA 1620  
Db 1739 TAAAGATGGTGATGATCAACCTTGGCCACTTTAATGGAACCACTCTCCGGCCAGAA 1798  
Qy 1621 GTTCACCTGGGCTGCCAGCTTCTCATATAGTTTTTTTGTGATAAGAAATGCCAAAGTTG 1680  
Db 1799 GTTCACCTGGGCTGCCAGCTTCTCATATAGTTTTTTTGTGATAAGAAATGCCAAAGTTG 1858  
Qy 1681 CTGCTTGATCTGAAAATAAATAATATACCTAGTCTGACACTG 1721  
Db 1859 CTGCTTGATCTGAAAATAAATAATATACCTAGTCTGACACTG 1899

## RESULT 15

AAA75053  
ID AAA75053 standard; cDNA; 1899 BP.  
XX  
AC AAA75053;  
XX  
DT 15-JAN-2001 (first entry)  
XX  
cDNA encoding a human heparanase polypeptide.  
DE  
XX Human; heparanase; gene therapy; tumour; inflammation; autoimmunity;  
XX heparin-binding growth factor; cytokine; neurodegenerative plaque;  
KW wound healing; infection; burn; angiogenesis; restenosis;  
KW atherosclerosis; inflammation; neurodegenerative disease;  
KW Gerstmann-Straussler Syndrome; Creutzfeldt-Jakob disease; ds.  
XX  
OS Homo sapiens.  
XX  
XX Key Location/Qualifiers  
FH CDS 94..1872  
FT /\*tag= a  
FT /product= "heparanase"  
XX  
PN WO200052178-A1.  
XX  
XX 08-SEP-2000.  
XX  
XX 14-FEB-2000; 2000WO-US003542.  
XX  
XX 01-MAR-1999; 99US-00258892.  
XX  
XX (INSI-) INSIGHT STRATEGY & MARKETING LTD.  
XX (HADA-) HADASIT MEDICAL RES SERVICES & DEV.  
XX (PRIE/) FRIEDMAN M M.  
XX  
XX Pecker I, Vlodavsky I, Feinstein E;  
XX  
XX WPI; 2000-579289/54.  
XX P-PSDB; AAB08850.  
XX  
XX New polynucleotides encoding a polypeptide having heparanase activity,  
XX useful in wound healing and in gene therapy, particularly in treating  
XX tumor, inflammation, autoimmunity, neurodegenerative diseases.  
XX  
XX Claim 9; Page 121-122; 152pp; English.  
XX  
XX The present sequence encodes a human protein with heparanase catalytic  
XX activity. The heparanase (hpa) polynucleotide is useful in gene therapy,  
XX particularly in treating tumour, inflammation or autoimmunity.  
XX Particularly, the polynucleotide is useful in modulating the  
XX bioavailability of heparin-binding growth factors, cellular responses to  
XX heparin-binding growth factors (e.g. bFGF) and cytokines (e.g.  
XX interleukin (IL)-8), cell interaction with plasma lipoproteins, cellular  
XX susceptibility to certain viral and some bacterial and protozoa  
XX infections, or disintegration of neurodegenerative plaques. The  
XX polynucleotide is also useful in wound healing (e.g. thermal, chemical or  
XX radiation burns), and in the treatment of angiogenesis, restenosis,  
XX atherosclerosis, inflammation, neurodegenerative diseases (Gerstmann-  
XX Straussler Syndrome or Creutzfeldt-Jakob disease), and some viral,  
XX bacterial or protozoa infections  
XX  
XX Sequence 1899 BP; 495 A; 433 C; 510 G; 461 T; 0 U; 0 Other;

Query Match 99.8%; Score 1717.8; DB 3; Length 1899;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1719; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Qy 1 CTAGAGCTTCGACTCTCCGCTCGCGGACGCTGGCGGGGGAGCAGCCAGGTGAGCCCA 60  
Db 179 CTAGAGCTTCGACTCTCCGCTCGCGGACGCTGGCGGGGGAGCAGCCAGGTGAGCCCA 238

Qy	61	AGATGCTGCTGGCTCGAAGCCTGGCTGCGCGCGCGCTGATGCTGCTCTCTGGGC	120
Db	239	AGATGCTGCTGGCTCGAAGCCTGGCTGCGCGCGCGCTGATGCTGCTCTCTGGGC	298
Qy	121	CGCTGGGTCCCTCTCCCTCGGCGCCTGCCGACCTGCGCAGCAGCAGGACGCTGTGG	180
Db	299	CGCTGGGTCCCTCTCCCTCGGCGCCTGCCGACCTGCGCAGCAGCAGGACGCTGTGG	358
Qy	181	ACCTGGACTCTTCCACCCAGGAGCGGTGCACTTGGTGAGCCCTCGTTCCTGTCCGTCA	240
Db	359	ACCTGGACTCTTCCACCCAGGAGCGGTGCACTTGGTGAGCCCTCGTTCCTGTCCGTCA	418
Qy	241	CCATGTGACGCCAACTCTGGCCACAGGACCGCGGTTCTCATCTCTCGGTTCTCCAAAGC	300
Db	419	CCATGTGACGCCAACTCTGGCCACAGGACCGCGGTTCTCATCTCTCGGTTCTCCAAAGC	478
Qy	301	TTCCGTACTTTGGCCAGAGGCTTGCTCTCTGGTACCTGAGGTTTGGTGGCACCAGACAG	360
Db	479	TTCCGTACTTTGGCCAGAGGCTTGCTCTCTGGTACCTGAGGTTTGGTGGCACCAGACAG	538
Qy	361	ACTTCTCAATTTTCGATCCCAAGAGGAATCAACCTTTGAAGAGAGAAGTTACTGGCAAT	420
Db	539	ACTTCTCAATTTTCGATCCCAAGAGGAATCAACCTTTGAAGAGAGAAGTTACTGGCAAT	598
Qy	421	CTCAAGTCAACAGGATATTTGCAAAATATGGATCCATCCCTCTCTGATGTGGAGGAGAAT	480
Db	599	CTCAAGTCAACAGGATATTTGCAAAATATGGATCCATCCCTCTCTGATGTGGAGGAGAAT	658
Qy	481	TACGGTTGGAATGCGCCCTACAGAGGCAATTTGCTACTCCGAGAACTACACGAGAAAAGT	540
Db	659	TACGGTTGGAATGCGCCCTACAGAGGCAATTTGCTACTCCGAGAACTACACGAGAAAAGT	718
Qy	541	TCAAGAACAGCACCTACTCAAGAGCTCTGTAGATGTCTATACATTTTGCACAACTGCT	600
Db	719	TCAAGAACAGCACCTACTCAAGAGCTCTGTAGATGTCTATACATTTTGCACAACTGCT	778
Qy	601	CAGGACTGGACTTGATCTTTGGCCCTAAATGCGTTTATTAAGAAACAGCAGATTTGCAGTGG	660
Db	779	CAGGACTGGACTTGATCTTTGGCCCTAAATGCGTTTATTAAGAAACAGCAGATTTGCAGTGG	838
Qy	661	ACAGTTCTAATGCTCAGTTGCTCTCGACTACTGCTCTTCCAGGGGTAFAACAATTTCTT	720
Db	839	ACAGTTCTAATGCTCAGTTGCTCTCGACTACTGCTCTTCCAGGGGTAFAACAATTTCTT	898
Qy	721	GGGAACTAGGCAATGAACCTTAACAGTTTCTTAAAGAGGCTGATATTTTCATCAATGGT	780
Db	899	GGGAACTAGGCAATGAACCTTAACAGTTTCTTAAAGAGGCTGATATTTTCATCAATGGT	958
Qy	781	CGCAGTTAGGAGAGATTTTATTCAAATGCAATAAATCTTAAGAAAAGTCCACCTTCAAAA	840
Db	959	CGCAGTTAGGAGAGATTTTATTCAAATGCAATAAATCTTAAGAAAAGTCCACCTTCAAAA	1018
Qy	841	ATGCAAAACTTATGGTCTGATGTTGGTCHAGCCTCGAAGAAAGACGGCTAAGATGCTGA	900
Db	1019	ATGCAAAACTTATGGTCTGATGTTGGTCHAGCCTCGAAGAAAGACGGCTAAGATGCTGA	1078
Qy	901	AGAGCTTCTCGAAGGCTGGTGGAGAAGTATGATTAGTTACATGCAATCAGTACTATT	960
Db	1079	AGAGCTTCTCGAAGGCTGGTGGAGAAGTATGATTAGTTACATGCAATCAGTACTATT	1138
Qy	961	TGAATGGACGGACTGCTACCGAGGAAGATTTTCTAAACCCCTGATGTATTTGGACATTTT	1020
Db	1139	TGAATGGACGGACTGCTACCGAGGAAGATTTTCTAAACCCCTGATGTATTTGGACATTTT	1198
Qy	1021	TTTCATCTGTGCAAAAAGTTTTTCAGGTGGTTGAGAGCAACGAGCCCTGGCAAGAAGTCT	1080
Db	1199	TTTCATCTGTGCAAAAAGTTTTTCAGGTGGTTGAGAGCAACGAGCCCTGGCAAGAAGTCT	1258
Qy	1081	GGTTAGGAGAAACAGCTCTGCATATGGAGCGGAGCGCCCTTGCTATCCGACACCTTTG	1140
Db	1259	GGTTAGGAGAAACAGCTCTGCATATGGAGCGGAGCGCCCTTGCTATCCGACACCTTTG	1318
Qy	1141	CAGCTGGCTTTTATGCTGGCTGGATAAATTTGGGCTGTGTCAGGCCGAATGGGAATGAAGTGG	1200

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Search completed: February 28, 2006, 05:05:55  
Job time : 1074 secs